



Docket No.: CL001188
Serial No.: 09/817,198
Inventors: YE, Jane et al.
Title: ISOLATED HUMAN RAS-LIKE PROTEINS...

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1  TGCCCCGCTGC CCGCCCCGAG TTCCCCGGCCC CGCTGGCCCC AGTCATGGCG
51  AAGCAGTACG ATGTGCTGTT CCGGCTGCTG CTGATCGGGG ACTCCGGGGT
101 GGGCAAGACC TGCCTGCTGT GCCGCTTCAC CGACAACGAG TTCCACTCCT
151 CGCACATCTC CACCATCGGT GTTGACTTTA AGATGAAGAC CATAGAGGTA
201 GACGGCATCA AAGTGC GGAT ACAGATCTGG GACACTGCAG GGCAGGAGAG
251 ATACCAGACC ATCACAAGC AGTACTATCG GCGGGCCAG GGGATATTTT
301 TGGTCTATGA CATTAGCAGC GAGCGCTCTT ACCAGCACAT CATGAAGTGG
351 GTCAGTGACG TGGATGAGTA CGCACCAGAA GGCGTCCAGA AGATCCTTAT
401 TGGGAATAAG GCTGATGAGG AGCAGAAACG GCAGGTGGGA AGAGAGCAAG
451 GGCAGCAGCT GGCGAAGGAG TATGGCATGG ACTTCTATGA AACAAAGTGCC
501 TGCACCAACC TCAACATTAA AGAGTCATTC ACGCGTCTGA CAGAGCTGGT
551 GCTGCAGGCG CATAGGAAGG AGCTGGAAGG CCTCCGGATG CGTGCCAGCA
601 ATGAGTTGGC ACTGGCAGAG CTGGAGGAGG AGGAGGGCAA ACCCGAGGGC
651 CCAGCGAACT CTTGGAAC CTGCTGGTGC TGAGTCCTGT GTGGGGCACC
701 CCACACGACA CCCCTCTTCC CTCAGGAGGC CCGTGGGCAG ACAGGGGAGC
751 CGGGGCTTTG CCCTGCTGCT GTCTCTCTGT GTGATGACCC TATTGAGTAT
801 CAGTAGCCAC TACTCCCCCT GCCTGGCCCT GAGAGCGGCT CTGCTGTCAT
851 CTCAAGCAGC CCCTGTCCCC AGCCCCGCCA CCCTGGAGTG GTCTTCTTCA
901 GCCTGTTTCC CCAGCCACAG GCCTGCTACG ACCCCACGCA TGTGCCGCAA
951 GCACTGTCTC ACCATCCGCG ACCCACCAGA CAACAGCCAG GGCTGGAGTC
1001 CAGGCCACTT TCAGCTGCTC CTTTCTCCGT GCATCGTGTC TCTTCTCTGC
1051 TTTTCTCTC TTTCCCACT TCTTCTCTC TGACCCCTCC CCTCCGGTGC
1101 GTTTCGTATC AAAGCTCCTC AAACCCCGTC CCCCCTGTGT CCTGCTGTGT
1151 GCAGCTCGCT CTTTCTTCC TTTCTAAGCT ATCCAAGGGG ATGGACCCAG
1201 GCTCGTGGGG AGGTTCACCC CTTGGATCCA GGAAGAACCC TCCACCCTGC
1251 CTCGTGGGTG GGCCAAAGGC TACAGGGTGC TTCTTCTCT TCCCCACCC
1301 CCACTGTCCC TCATGTGCCA TGGGCCTGCC TCCCCAGTGA CCTGCGAAAG
1351 TGGAGCATCG AGGTAGGAGG GAAACAGCAA CCGGGGAGTC CTCGAGCCTG
1401 GGGCTGCCCT ACCTCTACCC ATTCCCGAC CAGAGCTTTG CCCTTGCTTG
1451 GCTGCCCGCC TGCTCTTTG GGGAACTGAG CTCAGAGGCA GGTGCTTCAG
1501 AGAAGGAAAC AAAATGAGGG GTGGCAGGGA TAAAAGTCA CCTCCATTCT
1551 CTACCTCCCA TGCAGCATGA ACACAATTTC TCTCCACCTG GCTCCCAAAT
1601 TTAAAGATGT GGACCAAGGC CTGTGGGTAC TCCAGGGGCA AGGAGAGCCC
1651 TGGGGTCAGT GACACTGTCA GGCCAACCAT GCAC'TCCACA AAGGGGAGCA
1701 TTTGGAATG AAGGACTAGC TCCTATGTAT CAGGTTAAGA GCAAGGGAGA
1751 GCTGGCCAGG GACAGCAGTT TGCACAGCAG AGGGGAATGT AGCAACAGCA
1801 GGGCCTCCTA GGCCCCATCT TCCATTCTT AGGTAAGAAG AGCATTTCCT
1851 CAGACTCCCA GGCGGAGGAC TGAGCCTAGC CTTAGCAAC CAAGGTTCTC
1901 CTGGGACCCA AAGTTTATGG GAGAAGGGCA AAGACTTCAT GGAAGAGAG
1951 AAGGAAGGCC CTGGGTAGAA ACGCTTGGTG CTGTTCTCTT TGGCCTTAA
2001 GACAAAGCGC TCATCTTGCC CTCTACCTCC TGATAGGCTT GAGGGTTTGC
2051 CAACCACACT GTGGCTACAG GTGGAGGGAA GAGGACTCCT TCCTCCAGAG
2101 TGCTATGTTT AGGAAGTTTC TTTAACCCCA TATGGCCCAA GAGTAGCTCG
2151 TAGGAGGCC TTTAAAGACG GAACAAGTAA TTTACCAATT CACTGGGGT
2201 TCCTGCCCAC CGTCCCAAGG TGGGCGAGGC CTAGGAAGAG GGTCACTCTT
2251 AAGCCACACA TTAGCTGCAC TGCGTGGCTG CAGCCAAAAC AAAGAACTGG
2301 GTGTTGAGTA TTCATCAACT AAGAACCAAA ATCCAGGGCA CTCATATGTG
2351 AAGGATAAGA ACCTCACTTC CTTACTCTC CAAAAAGAAG TGGGAAAGA
2401 ACCATCAAAC CTTTCTCTCT GACTTACCAA ACCAGGAAA CAGCAGGAGA
2451 GGGTGGCTCA GGACTTAGGG ACAGGGTATA GCTTAGATGG TGGAAAGCAA
2501 AGGAGAGCAG GAAGTTGTAA ATCACTGGCT AATGAGAAAA GGAGACAGCT
2551 AACTCTAGGA TGAAGCTGTG ACTAGGCTGG AGTTGCTTCC TTGAAGATGG
2601 GACTCCTTGG GTATCAAGAC CTATGCCACA TCACACTGGG GCTAGGGAAG
2651 TAGGTGATGC CAGCCCTCAA GTCTGTCTTC AGCCAGGGAC TTGAGAAGTT
2701 ATATTGGGCA GTGGCTCCAA TCTGTGGACC AGTATTTTCA CTTTCCCTGA
2751 AGATCAGGCA GGGTGCCATT CATTGTCTTT CTCTCCTAGC CCCCTCAGGA
2801 AAGAAGGACT ATATTTGTAC TGTACCCTAG GGGTCTGGA AGGGAAACA
2851 TGGAATCAGG ATTCTATAGA CTGATAGGCC CTATCCACAA GGGCCATGAC
2901 TGGGAAAAGG TATGGGAGCA GAAGGAGAAT TGGGATTTTA GGGTGCAGCT
2951 ACGCTCACCC TAAACTTTTG GTGGCCTGGG GCATGTCTTG AGGCCAGAC
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FIGURE 1A



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3001 TGTTAAGCAG GCTCTGCTGG CCTGTTTACT CGTCACCACC TCTGCACCTG
3051 CTGTCTTGAG ACTCCATCCA GCCCCAGGCA CGCCACCTGC TCCTGAGCCT
3101 CCACTATCTC CCTGTGACGG GTGAACTTCG TGTACTGTGT CTCGGGTCCA
3151 TATATGAATT GTGAGCAGGG TTCATCTATT TTAAACACAG ATGTTTACAA
3201 AATAAAGATT ATTTCAAACC ACCAAAAAAA AAAAAAAAAA AAAAAAAAAA
3251 AAAAAAA (SEQ ID NO:1)

FEATURES:

5'UTR: 1-44
Start Codon: 45
Stop Codon: 681
3'UTR: 684

Homologous proteins:

Top 10 BLAST Hits

	Score	E
CRA 335001101587561 /WO200058473 /org=Homo sapiens /taxon=9...	428	e-119
CRA 18000004937398 /altid=gi 464561 /def=sp P35289 RB15_RAT RAS...	423	e-117
CRA 18000005187045 /altid=gi 7498104 /def=pir T33855 hypotheti...	220	6e-56
CRA 18000004929618 /altid=gi 131798 /def=sp P24407 RAB8_HUMAN R...	216	1e-54
CRA 335001098683352 /altid=gi 11422744 /def=ref XP_001482.1 TR...	214	4e-54
CRA 18000005096141 /altid=gi 2317272 /def=dbj BAA21744.1 (AB00...	214	4e-54
CRA 18000004952869 /altid=gi 131848 /def=sp P22128 RAB8_DISOM R...	212	3e-53
CRA 335001098688905 /altid=gi 11432830 /def=ref XP_007682.1 RA...	211	4e-53
CRA 18000004945380 /altid=gi 131847 /def=sp P22127 RAO1_DISOM R...	211	5e-53
CRA 18000005163099 /altid=gi 7705849 /def=ref NP_057215.1 ras-...	210	6e-53

BLAST dbEST hits:

	Score	E
gi 12333507 /dataset=dbest /taxon=96...	626	e-177
gi 12120217 /dataset=dbest /taxon=96...	377	e-102

EXPRESSION INFORMATION FOR MODULATORY USE:

library source:

From BLAST dbEST hits:

gi|12333507 brain

gi|12120217 epid_tumor

From tissue screening panels:

Fetal whole brain

FIGURE 1B



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1 MAKQYDVLFR LLLIGDSGVG KTCLLCRFTD NEFHSSHIST IGVDKMKTI
51 EVDGIKVRIG IWDTAGQERY QTITKQYYRR AQGIFLVYDI SSERSYQHIM
101 KVVSDVDEYA PEGVQKILIG NKADEEQKRQ VGREQQQLA KEYGMDFYET
151 SACTNLNIKE SFTRLTELVL QAHRKELEGL RMRASNELAL AELEEEEGKP
201 EGPANSSKTC WC (SEQ ID NO:2)

FEATURES:

Functional domains and key regions:

[1] PDOC00001 PS00001 ASN_GLYCOSYLATION
N-glycosylation site

205-208 NSSK (SEQ ID NO:6)

[2] PDOC00005 PS00005 PKC_PHOSPHO_SITE
Protein kinase C phosphorylation site

Number of matches: 2

1 92-94 SER
2 206-208 SSK

[3] PDOC00006 PS00006 CK2_PHOSPHO_SITE
Casein kinase II phosphorylation site

Number of matches: 2

1 29-32 TDNE (SEQ ID NO:7)
2 104-107 SDVD (SEQ ID NO:8)

[4] PDOC00007 PS00007 TYR_PHOSPHO_SITE
Tyrosine kinase phosphorylation site

101-109 KVVSDVDEY (SEQ ID NO:9)

[5] PDOC00008 PS00008 MYRISTYL
N-myristoylation site

Number of matches: 2

1 18-23 GVGKTC (SEQ ID NO:10)
2 136-141 GQQLAK (SEQ ID NO:11)

[6] PDOC00017 PS00017 ATP_GTP_A
ATP/GTP-binding site motif A (P-loop)

15-22 GDSGVGKT (SEQ ID NO:12)

[7] PDOC00579 PS00675 SIGMA54_INTERACT_1
Sigma-54 interaction domain ATP-binding region A signature

11-24 LLLIGDSGVGKTCL (SEQ ID NO:13)

FIGURE 2A



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BLAST Alignment to Top Hit:

>CRA|18000004937398 /altid=gi|464561 /def=sp|P35289|RB15_RAT
RAS-RELATED PROTEIN RAB-15 /dataset=nraa /length=212
Length = 212

Score = 423 bits (1077), Expect = e-117
Identities = 207/212 (97%), Positives = 209/212 (97%)
Frame = +3

Query: 45 MAKQYDVLFRLLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMTIEVDGIKVRIQ 224
MAKQYDVLFRLLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMTIEVDGIKVRIQ
Sbjct: 1 MAKQYDVLFRLLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMTIEVDGIKVRIQ 60

Query: 225 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 404
IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG
Sbjct: 61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120

Query: 405 NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQHRKELEGL 584
NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQHRKEL+GL
Sbjct: 121 NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQHRKELDGL 180

Query: 585 RMRASNELALAELEEEEGKPEGPANSSKTCWC 680 (SEQ ID NO:2)
R ASNELALAELEE+EGK EGPANSSKTCWC
Sbjct: 181 RTCASNELALAELEEDEGKTEGPANSSKTCWC 212 (SEQ ID NO:4)

>CRA|335001101587561 /dataset=GENESEQ /org=Homo sapiens /taxon=9606
/mol_type=protein /date=08-FEB-01 /length=218
/altid=derwent_id|B41604 /altid=derwent_ac|B41604
/def=Human ORFX ORF1368 polypeptide sequence SEQ ID
NO:2736 /patent=W0200058473-A2 /pat_section=Claim
Length = 218

Score = 428 bits (1088), Expect = e-119
Identities = 212/218 (97%), Positives = 212/218 (97%), Gaps = 6/218 (2%)
Frame = +3

Query: 45 MAKQYDVLFRLLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMTIEVDGIKVRIQ 224
MAKQYDVLFRLLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMTIEVDGIKVRIQ
Sbjct: 1 MAKQYDVLFRLLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMTIEVDGIKVRIQ 60

Query: 225 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 404
IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG
Sbjct: 61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120

Query: 405 NKADEEQKRQVGREQGQ-----QLAKEYGMDFYETSACTNLNIKESFTRLTELVLQHR 566
NKADEEQKRQVGREQGQ QLAKEYGMDFYETSACTNLNIKESFTRLTELVLQHR
Sbjct: 121 NKADEEQKRQVGREQGQKCPSLQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQHR 180

Query: 567 KELEGLRMRASNELALAELEEEEGKPEGPANSSKTCWC 680 (SEQ ID NO:2)
KELEGLRMRASNELALAELEEEEGKPEGPANSSKTCWC
Sbjct: 181 KELEGLRMRASNELALAELEEEEGKPEGPANSSKTCWC 218 (SEQ ID NO:5)

FIGURE 2B



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Hammer search results (Pfam):

Model	Description	Score	E-value	N
PF00071	Ras family	323.8	8.2e-95	1
CE00060	CE00060 rab_ras_like	211.0	1.8e-59	1
PF00006	ATP synthase alpha/beta family	4.2	2.1	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
PF00006	1/1	10	24 ..	203	217 ..	4.2	2.1
CE00060	1/1	2	165 ..	16	184 ..	211.0	1.8e-59
PF00071	1/1	10	212 .]	1	198 []	323.8	8.2e-95

FIGURE 2C



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1 GCTCAAGATT GCACAGCTGG TGAGTGGTGA CACTGGGACT GGAACCCAAG
51 TGTGCCTTAC TCCAGAGCCC TTGGCATGCA CCTGAAACCC CATGTAAGCC
101 CACTGTGGAG ACGCGCACCT CGAAATAATG GAATCCACTA CATCAGTTCC
151 TTTAGCTTTC TGTGTAATCA GAGTAGCTAG CAGGCTCGGG ATTTGCCCCC
201 CCGGCTTTTT TTTTTTTTTT TTTTGTAGAC AGAGTTTTGC TCTTGTGGCC
251 CAGGCTGGAG TGCAATGGCG CAATCTCGGC TCACCGCAAC CTTGCGCTCT
301 CAGGTTCAAG CAATTCTCCT GCCTCAGCCT CCCGAGTAGC TGGGATTACA
351 GGCACCGGCC ACCACGCCCA GCTAATTTTT TTATATTTTT AGTAGAGATG
401 GGGTTTCACC ATGTTGGCCA GGCTGGTCTT GAACTTTTCC CCTCTTATTA
451 TAATTCAGAC ACTTAACCTG AAATATACCT TTTCAAATGA AGTAAATGGG
501 CTTACCACTT TCCTTGACCT ACTATTGAAA AATACATTCT CCATCCAATA
551 TTCAGCCTGA AAACAGGTAT GTACATATAT ACTTTTCATT GCTTTTTTTT
601 TTTTTTTTTT GAGACAAGGT CTCCCTCTGT TGCGCAGGCT GGAGTGCAGT
651 GTCATGATCT CGGCTCACTG CAGCCTTCCC CTAATGGGTT CAAGCAATCC
701 TCCCACCTCA GCCTCTCAAG CCTGGGATTA CAGGCGAGCC ACCGTGCCCA
751 GCTAATTTTT TTTTATTTTT AGTAGAGACT GGGTTTCACT ACATTGGCCA
801 GGCTGGTCTC CAGCTCCTGA CCTCAAAGTG ATCTGCCCCG CTCAGCCTCC
851 CAAAGTACTG GGATTACAGG CATGAGCCAA CGCGCCTAGC CTTTCATGTC
901 TTTTTTAAAG CCTAATAGGC TAGACTTTCG TCTCCCTCAA TACTCGTTGG
951 TAGGGATAGG CAATTTTCTC AACTCCGGAG AGCATTTCATT TGCCTCTCTC
1001 CGGTGCTAAC ACATTCAGTG GTAGGAAACT GGATCTTGAA CAAGGGCCAT
1051 TCATTCTTTG GTGCCACTGG CTATACCACA GAGAAATTTA GGGGTCTGAA
1101 ACAATACATT GGTCACCTGG GCACCTATCC TAAGCACCTT AGAGGGAAAA
1151 CGGAGACTTG CCCGCACACC TCTAAAGGAT TTTGCACTTG GAGATGTTCT
1201 TATGGCCATC TATCTTTTCA CCCTGGTGGA GGCCGTGAAT AGGCATTTTC
1251 CCCATTTAAA GAAAAAATGG GGACGGGGGA GGGCCGTGAC ACAGTCACAC
1301 AGGTAAGGGG CAGCCAGATG GCAGGGAGGG GGAATTCCAC CCACACTCTC
1351 GGGGACTCAT GGAGACGGGT GTTCGAATCC AGATCCTGCT CAAGGCCTTC
1401 CTACCTCGGG TGAGCCAGC TGAGGTACCA GCCACTGGGG AGCCCCGCCA
1451 GATCCTGCAG ATGCAGGGTG CCACGGCGGG CGGAATTACC GGCGCCAGAC
1501 TTGGGGTGGG ATATGGGGAG AAGTGGTGAG CCCGAAAAGC GGAGCACGGT
1551 AGAAGTGGGC TGGGTGGGGG CTCACCTCAA CTCCCCCATT CGGAGCGTCC
1601 GCGGAAAAAC GAAACGTTT CCCC GCCCGG GGCAGGAAGG GGTGAGGAGG
1651 GGGGGCTGGC GCCCCGCCCC AGCGTCGCCT GCTCGATGGG GTCCCGCTCT
1701 CCTGCGCGCG CTCCCCGCC CCTCTCTACC GGGGCGGCGG CGGCGGCGCA
1751 GGGGAAGGGG CGGGCAGGGG CCGCCGCCGG TTTCTCTCC CACCGCCTCG
1801 CGCCAGCCCA GCGGAGCCGA GCGGAGCCGA GCGGGCGCGG CGCCGGGCTC
1851 CCGCCGAGC GCGCTTCCC GGCACCCAGC GAGCGAGTGG GCAGGCGGGC
1901 GGGCGAGGCA GCGCGGGGG CCGGGCCCGG CGTCCTCTC GCCGCCGCA
1951 GCGTCCCCGG GCGGGCGCGG GCGCGATGG CAGCGGCGGA GCAGGGCTGA
2001 GCGCGTGCC GCGCCGAGT TCCCGGCCCC GCTGGCCCCA GTCATGGCGA
2051 AGCAGTACGA TGTGCTGTTC CGGCTGTGTC TGATCGGGGA CTCCGGGGTG
2101 GGCAAGACCT GCCTGTGTG CCGCTTACC GACAACGAGT TCCACTCTCT
2151 GCACATCTCC ACCATCGGTA AGGGGCGGTG GCGGGGGCG CCCCTCCCTC
2201 CCGCCCGCGG GCGCTTTCC CCGCCGCCCC CGTCCCGAGC TGGGGAGGAA
2251 TTGCCAGCCC CTCCGGCTGG AGGCGGTGGC GCGGAGGCC GGAGTCCGGG
2301 ATAAATCTCG GGGTGAGCAT AGGTTTTGGC AGGTGAGGGT GTCCCTGCTG
2351 CCTGCCGTCC GGACCAGGGG TGGGGTCTCC CGCCTCTTGC CGGGAAGCCT
2401 TCCGTCCCAT CAAACCGAGA AACCAGGGGT GAGGGGAGCT GGTGTAGGCC
2451 TGGGTACCCC GAGCTGGGGT AGCAAGAATC GTAGCCGCTG GAATAACACC
2501 CCCACACCCC CAGGGGGAGG GGAAGTAAAG CTTCTGCTAC GGAAAAGGGG
2551 GTCAGGGTGG AGACCGGAGT CACTGAGGCG CCCTTGTTTC TGTGGTGACC
2601 CAAGGTGGAG CCGGCGGGGG GCGAGGGGGG GAAGAGAGGA CGTACGGAGG
2651 GGCCACAGGG ATCGAGTTTC CAGGGCAGAG TTGGGAAGGT AAGCCGCAAG
2701 GTGGGACACC TGGGGGAGGA CACAGATAGG GTGAGGAGCC CCTGCGCCTG
2751 GGAAGAGGAG ACATCTGTTC TGAGGGAGGC TAAAGAGGAT GGAGGAGTGT
2801 CAGGAATACC TGCCCAGACC AAGGGGTCAG AAGGCAGGCA GGACCCGCCT
2851 GAGGCATCT CTCATCTGGC AGTGCTGGAG CCTGTGGTTA GAGGGACAAG
2901 ACCCGGTGGC ATCCAGACA GCACTATGAT GGGGTCACTT ATTCTAGGAA
2951 TGGGTCCATG GCCTCCCCCTC TGAGACAGTC AGTCTCCCGC TTCTAGGCTG
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FIGURE 3A



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3001 TGAGGGGGCCC CCTCCCTGAG AAGTCTGAGT AGAGGGAATT TCATCCTCAG
3051 CTGCTACCCG GGTCAGCCCT GGAGTAGCCT CTGCATTGCC CAAGCCCTG
3101 GAAACACCTG CTGGCTGGCT GGTCATCCAT TTGGAATGCT CTCCTAGAAG
3151 TCCCTGCTGC CATCAGGGAT GGGCACCAGC TCTCAGCTTC CTCTTGAGGA
3201 TTCATGTGCA CACCATCCCC CCTCCCCCA ACACACATTC CTTGCTGAGA
3251 GAGAAGTAGG AGCAGATAGA TACAGCCAGG AGGAACAGAA CCTTCTGGTT
3301 AAGAAGCCAG CTTTATTGTC CAAGAGACCT GAGACCTCAC TGTGGGGCAA
3351 AGCAACCTTG AATATTGCCT AAACCTTCTGA GCTTTATTTA GTTTCTCATC
3401 TGTAGAAGCG GTATAATAAT TGCACCTACC TGCCAAGTTG TTGTCAAGAT
3451 TAAATGAGAT AACGATTGTT AAGTGCTTAG CACAGCCAGA CACATGGTGA
3501 AGCTCGATAA ATGCTGATTG TTCTTACTGC TATTGCCATT ATCATTGAGC
3551 TTTTAGGGTG TCCTCTCTTT GTTTCACCAA CTTGAAGGGT GAAACAACAG
3601 GACTTAGGGT CAGGGAACAG AACTTGTCCTG TCTTTCTCAG AGGAGCTGTA
3651 AGGCCAACTC TTAGGAAACC CAGGAGCTTG GGCTGAGCCA TGGTTTGGAT
3701 GAGAGACATT GCAGAAAGAA GGGGAGCCTA TAGACACTAA GGCTTTGTGC
3751 CTGCCGGGAG GACTTGGGGA AGAGGCAGGT GCAGGAGAAA GGCAATGGCG
3801 TGATGGAGGA AGTGGCAGAG GAACCAGATG GTGTATGAGG ACAGGTTGTG
3851 GGCTCAGGGA CAAAGGGCGG TGGGTTATCC CTTAAGGAAA CTAGGAGTGG
3901 CTATTTTGGG GAGAGGCTG GTGCTTGGA CTAAGGAGCT ATCTCCAGAG
3951 AGCTGTGGGC TGCTTGGGAG GCCCTGGCTT TGGCCTGAAG AGCTGTTGTT
4001 TGCACCTGCT CTCCTAGTCC CATTCCAAGT CCTATAGGTG ACATGGACTT
4051 TTCCCTTTGA GGGCTTCATT CAACCACCTC ATTTCAGAAG CTCTGGGACT
4101 CCTGCTTAGT GCTGTGGGAG GCAGCCTCCC CTGGGAGACA CATACCCTCC
4151 TTTTGTAGGG CACCCCTCTT TCTAAAATAC CAGGATGGCC CTCTGAGGCT
4201 CGTGCTCTCC TTAAGAGAG TCCATTGCCT CACACCTCTA ATCATCCACC
4251 CTTCTCCCTG TCCCTTCCCC TTGTAATCTC CTTTCTTAGA CACCTTCTGC
4301 TAATAGGTGA ACATAAATA GGTCACAGGG ACTTCCTGAA ACCCTCCAGG
4351 GCAGACCACT TTGGGCACAT AGGTGAATCA GTGAAGTGA TAGGGGTGTC
4401 TCTGCAGCAC TGTCTCCCTT CAAGGCCCTT GGTATATTGG CCTAAAACCT
4451 AAAGATGGCT CCCAGATTTC TTCCTCCGCT TCTGACACCC GGGTTCCCCT
4501 TTCTACAGGA CACAGAGGAT TCTTAGGGT CCCCCTTCC ACAGGACACA
4551 GAGGACTCTA GGAGTTTGA TTCCATGGAA TAGAAAAGAAA CCTGTCTTTC
4601 TTCACACCAG CTTTTTAAAA TCTGCCCCAC TGGGTATCTT AAATGCTTTC
4651 TTATTTAAAG CTTATTAAAG GACTTGGGAT TCTCCCTTAT CTTGGGCGTG
4701 TTTTTCAGCA TTAATAAAA CTAAAGGAA AGAGTTGGAT GGTCAGAAA
4751 AGCTTTTTC TTAAGTGATA TGGACAGTTT CTCAAGGAGG TAGAAGGGGC
4801 AGCCAGGAGA CAAATCAAGG AGCCAACGAA ATGAGTGCTA CCAAGTCATA
4851 GTCATTGCTT TATTTTAAA AAATGCGTGT CCTGTATGCC AGGCTCTGCA
4901 CTGAGACCGA GAGATTCCAA GATGAATAAT ACCTACAGTC ACTGTTCTCA
4951 AATTGTGCAT TACCTAAAAC ACATTACATG ACCATGCTGG CCACTGATCG
5001 AGGCACCTTT CCCAGGGGCT TTTTTTGTGA ATTAAGAAAA CAAGGTAATT
5051 CACCAGTTAT TGCCAAGATA GTTTGGCTTC TTGGCTCATG TGGATATCAC
5101 CTAGGCCAGT ACTTTTGTGA TTTACTGTGT ACTCCACTTT AACGGCCTGC
5151 GATCTTCTAG AGAAGAACCC GCCAGGGAGC AGTGAGAGGC CTCCCTGGTA
5201 GACTGAGACA GACTGTGCTT CTCCCCTAT CTTTTCTGTC TTTCTGGCCA
5251 GCAGACCAGC AGGTGGCCCT GCCACTGCTT CTGCCACAGG CATTTCCTTT
5301 CTGTGCAGCT GTGCTGGCCT GGCTGGGGGT TGGTGCGAAG GGGTCCCCAA
5351 AATACTACCT TAAACAAATT AATTGAGCAT TCACTACCAA GCTCTGTGCC
5401 AGGCATTTTA GAGACATATT GCAGTCTACG TTTTCTGCCC ACAGAAGCCC
5451 ATAACCTAGA TGGGGAGGCA AGACAAAGGG AAAACAAAA AACAAAGAGC
5501 TAGTGCCAAA ATGAGATATC TGAAAGAACT TGGTGAATCA CTCTCAAAT
5551 GTAAAGGATG GATTATGATC ATTGCAGTTA CTCTTAATGA AGGTCTCACA
5601 GTGGGTATCA GAAGCTAAAT TATGATGCAA GATGTACCAT GAGGCAGCCG
5651 GAGAATGGCG ATGGATGGGA TGGGTGAGTG CTATTTCCAC GACTCCATGC
5701 TGTGCGAGGC TGGGGAAGAG AGAGGCCCTT GTGGACTAGA ACCGGCAGGG
5751 AAGGCTGAAG CTAGGCCCTCA GTGTGGGCTG CTCGTCAGTT CCTGCAGCAG
5801 AAGGGAGCAG ATGGAGTAAC ATGAGCAGAG ATAACAGAGG TGGGATTGAG
5851 TAGGTGTCCG TGGGGCTCTA GGCAGTTTAT ATGCAACAGA AGGGATTCTT
5901 CAGGAAAGTG AGAAGATTCT TCTGTTTCTC TCTCTGTCTC CCAAATTATA
5951 AGTGCCTTGA TGGTGCAGCC AAATCTTATT CCTCATTGTT TTTATAGTCC
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FIGURE 3B



Docket No.: CL001188
Serial No.: 09/817,198
Inventors: YE, Jane et al.
Title: ISOLATED HUMAN RAS-LIKE PROTEINS...

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6001 CTAGTACAGG GCCAGGCAGA TTCAATGCCT GTTGTTAAAT TAATGAATGA
6051 ATGCAGGGAC CAGTTGGCAG AGGGCATTGA GAGCCTGGCC AAGGAGGTGG
6101 AACATGAGCC TTAGCAATGG TAGGAGGGGT TTTGAGTAGG GTACTAATGA
6151 GGTTGGCTGG AAGAAGGGGT TAAGACTTGA AGCAGGGAGA CTAGTCAGGG
6201 GCTGCAGTAG TATCCTGGGC ATGAAGGAAC CTCTGAATGG CCCCTCACCC
6251 CCAGTGGTAC CAACACCAAC TTCCACACAG TCAGTTGTTT TACTTTCCCT
6301 CCAGAATGGG GAGTGGTTCA AGCCAATCAA CCTGGCAACT TCTGAAAGAA
6351 TCTTATGGGA CCTGTGCCAT GACCAGGTAG GGAGAAGATG TCATACATGG
6401 ACATCTATGT TCAGGGGACC TTTGAGGACC TTTCTGCATG GTGGCCAGGA
6451 GTGAGATGAT GTAAACCACA AATGGAACT GAAGAGACTG CTCAGGAGTT
6501 GTTGGTTTTT TTTTCTTTT TATTTTTTTT TTTTGTAGAC TAGGTTTCAC
6551 TCTGTACCC AGTCTGGAGT GTGGTGGTGG CACAATCAG GCTCACTGCA
6601 GCCTCGATCT CTTAAACGCA ATCCTCCAC CTCAGCCTCT CAAGTAGCTG
6651 GGAATACAGG TGCATGCCAC CACATTCAGC TAATGTTTGT ACGTTTTGTA
6701 GAGATGGGGT TTTACTATGT TGACCAGGCT GGTCTCGAAC TCCTGGACTC
6751 GTGATCCACC AGCCTCAGCC TTCCAAAATG CTGGGATTAT AGGCGTGAGC
6801 TACCTCACTC CCTCAGGAGT TGGTTTTCTC CCTCCCATCC TTAGTCTTCC
6851 CTGAGTAGAC CTGTCACTTA GTCCCTGGAC CTTTTGTTTT GAAAGCCACC
6901 CTCCAGGCTA CACTCCTTCT GGGTGAGGAG GAGGGTGATC TGGTTGGACA
6951 GGTTGGGGTG CTGTGGCTTC AGGGCACTTT CTCAGGCTGG GTTGCTGCTG
7001 CTATGTCACC TTTCTCAAGG AGTTCCTGCT GGACTGGCTT GGCTGCCTGT
7051 CTTGACTTTG CTTTTGACTG AGGAGGTGGG AGATGGTGAG GGAGGGGGTG
7101 GGGCTAGATC CAAGCCTGGA ATGGGGTGAC CTAACAGACA CTGGGGCCTG
7151 TGCTTAGACA CTAGGATCCT GGGGTTTTGA GGTTTCTAGA CTGAGAGGAG
7201 CTGGGGGCAA ATGCAGTGTG ACCTTGTGAG AGGGTCAGGG CTGGGTCTGT
7251 GTCAGCCTTC AGGCAGCCTG AGACCAGTCT CTACCTACTG TGTTCCTCTG
7301 GTACCTAGAA AGGAAGGGAA GGTGAGAAGC AATGAGCAGA ATGGAAAGAG
7351 CCCAGATTAA CATGCACATT TCCCATGGCC TTTACTGGCC TGTCACCTTC
7401 AGACACTTTG ATGACATCTT TGTGCTTCGT TTCTGCATCT GTAAATTGAA
7451 GATGGTAACA GAGTCTTTCT TAAAGTTGT TGTGAAGATT ATAGAGCTTA
7501 GCGCATATAA AGCACTTGGC AGAGCCCTCG ATAAATAAT AGCTGCTATC
7551 ATATTATCAT TATTATTATT TTATTATTAT ATTTATTAT TTTTTTTTGA
7601 GACCGAGTAT CTCTCTGTCG CCCAGGCTGG AGTGCACTGG CACAATCTCG
7651 GCTCACTGCA ACCTCCATCT CCCGGGTTTA AGTGATTCTC CTGCCTCAGC
7701 CTCCTAAGTA GCTGGGATTA CAGGCACCCA CCACCACACC CGGCTATTAT
7751 TATTATTCCT AGCTATAAGA ATGCTGTAGA GATGAATACA CTGTCAGTGA
7801 GCTAGGAGGT CATCCTGTGT ATCCATCACT TGTGCACTCA GTCGTTCAAG
7851 CGCTATTTGC TGAACACCAA CTACATGCCA GGTGCCATGC TAAGATTGAG
7901 GGACACAGTG GTGACCAAAA CAGACAGAAA CCAAGGAGCT GGCTTACATT
7951 CCAAGGGAGT GCATAGGAAG CTGTGTTTCA TTTCACTTTC TGCTCTAGTA
8001 CCCCCCTTTC CCTGGCAGTG CCAGGGTCTG AGAAGGAAGA GTGAGGTGGT
8051 GAGGAGGTGT GAAGCAGTGG GGTGACCTGA GAGGAGAGGA TGGGGTGGCT
8101 TTGCCTCAAG GCTTGGGCCC CTGCTAGGTG TCGCTCTGCC TCAGGCCTCT
8151 GTTTCTCCTC CTGACACAGG CACAGACTCG GCCTCCCACC CCTTCCCCAA
8201 GGACATGACC TTGGGAAGGA ACATATCTGA AGCCCGCGGA GGGTTTCCGC
8251 TGCTGTGCAT CTGTGCCACA GATCCGCAGA TGCAACCACA GCTGGGAGCA
8301 CCGGTTTCTC CCGCTACCT GCACTCCCTG GTTTCTGTTC CTTCTCCTC
8351 CTCCTTCTCT CTCCCCGCTC CCCAGACAGG CTGGTGATGA GCTTTATAAC
8401 ATGAAAGCTG ATATTTGGCC ATTATCCTTC TACCCTGATT GCCAGCTCTT
8451 CTCAGAGTGC CTTCTTCTGT AATCCAATCT TTGCACCACT TTCCCTGTGA
8501 AACTGCCAGT TTTCTGTATA GGCCTCTGCC CTCTCCTTGG CTCTTCTCTC
8551 TGGTCACTGA GCTTTGTCAA GGGGAACACA GGGCTTCTCT GACACGTAAT
8601 TCCTCCCACT GAGGAGGAAG GGGCTAATCA CCAGCCCTGT TTTATTTTAT
8651 TTTATTTTTT TGAGATGAAG TCTAGCTCTG TCGCCAGGC TGGAGTGCAA
8701 ATGGCTCGAT CTCGGCTCAC TGCAACTTCT GTCTCCCGGG TTCAAGCGAT
8751 TCTTCTGCCT CAGCCTCCTG AGTAGCTGGG GATTACAAGC ATGCACCACC
8801 ACACCTGGCT AATTTTTTGT GTTTTTAGTA GAGATGGGGT TTCACCATGT
8851 TGGCCAGGCT GGTCTCGAAC TTCTGACCTC AGCTGATCCA CCCACCTCGG
8901 CCTCCCAAAG TGCTGGGATT ACAGGAGTGA GCCACCATGG CTGGCCGACC
8951 CCATCTCTTA AAAAAACAAA AAGAAAAGAA AAGAAAACAA AACAAAAACA

FIGURE 3C



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9001 CTTTTTAAAT TAACTGATTA TGGTGGCATG TGCCTGTAGT CCTAACTACT
9051 CAGGAGGCTG AAGTGGAAAG ATTGCTTGAG CCCAAGTAGT TGGAGGCCAC
9101 AGTGAGCTGT GATCACACCA CTGTACTCCA GCCTGGGTGA CAGAGTGAGA
9151 CCCTGTCTCA GGAAAAAAAA AAAATTACTG AGAACTCTGT GACCATGGCA
9201 CCATGAACTA TAGAAAGGGC TAACAGTTGG CTTTGAAATG TGGGTTATGG
9251 CTGGGTGCCG TGGCTCACGC CTGTAATCCC AGCACTTGG GAGGCCAAGG
9301 TGGGCAGATC ACAAGGTCAG GAGTTTGAGA CCAGCCCGGC CAACATAGTG
9351 AAACCTCATC TCTACTAAAA ATACAAAAAA TTAGCCGGGT GTTGTGGCAG
9401 GTGCCTGTAA TCCTAGCTAC TCGGGAGGCT GAGGCAGGAG AATTGCTTGA
9451 ACCCAGGAGG TGGAGGTTGC CACAAGCTGA GATCGCACCA CTGCACTCCA
9501 GCCTGGGCGA CAGAGCAAGA CTCCATCTCA AAAACAAAAA TAAAAACAAA
9551 AAAAAGTGGT TTGTTTTCTT TTCTTTCTTT TTTCTTTT TT TTTT TTTT
9601 TTTTGAAACA GAGTCTTGCT CTGTCAACAG GCTGGATTGC AGTGGAGGAT
9651 CTCAGCACAC TGCCACCTCT GCCTCCCAGG TTCAAGTGAT TTCCCTGCCT
9701 CAGCCTCCAG AGTAGCTGGG ACTACAGGCA CGCACCACCA CGCTGGGCTA
9751 AGTTTTTGTA TTTTAGTACA GAAGGGGTTT CACCATGTTG GCCAGGATGG
9801 TCTCCATCTC CCTGACCTCG TGATCCGCCC ACCTCGGCCT CCCAAAGTGC
9851 TGGGATTACG GGCATGAGCC ACCACGCCCC GCCTAAAAGT GGGTTATTTT
9901 CTAATTGCTC TTCCCTGATT AAAATTTTCT CTTTGCCCAT CTTTTCTCTA
9951 GATATGTACT GACTTCATTC ATCCATTAT TCGTCTCACT TGCTCATTTA
10001 TTTTGTCTTT CATTTACTCT ACTTTGTTGA ATAATATTTA GTGATCTACC
10051 TGCTGCCAGG CAGTGAGAGT CTGAAGTGAA CAGGATGCTG CTTTGCCCTC
10101 TGGGAGCTTA CAGTGTAGCT GGGAAACAGA CATCCAAACA AGCAGAATAT
10151 TATGCAAAAG AAATGTCAGG ATGCTTTGGA ATCACAGAGG AGTGAGAAAT
10201 CCCTCCCGGG GAGGCTGGTG AAGGCTTTGA AGAGGAAGTG ACATTTGAGT
10251 GGAGTCTTGA AGACTAGGCA GGATTCTCCA GGGGCCCTGG GTGTGGGGGA
10301 AGCACACATC CTCTCCCTG TAGGAGGTGC TGTGGAGAAC ACCTCCAGTG
10351 GGGCTGCTAC TCTTCAGCCT TGCTGGGGCC AGCTGGAGTG GCCACACCAT
10401 GGTCACACCA GCTGAAGTTC AAGAAGCCCC TTGCCAGGAG ATTGCTTTGC
10451 TGGCTCTGGG TGAGGGCAGG TGCATCTGGA AGCCCCCTTC TTTCTAAGAT
10501 GTTTGCTCCT GAGTTTCTAT GTCCTAGTCT TTTCTTCCCT GAACCTTTTG
10551 CTACAGTCA GCACAGCCCT GCCTGAGAAG GAGGCTGGAG GAGTGAGTGG
10601 TCAGTAGCCT GGTGGGTCTT GGCTGCCTCT GTGGTGCCCG CTGGCCTAAG
10651 TAGCAGGCTT AGGGAGGCGA GACCCAGTTC CAGGGGCTGC CAATGGGGAG
10701 CGAGATGGGG TGGCTGGAGC ACACTGCACA TGTCACCAAG GCTCTAGGGA
10751 GGTCTGTGCA CAAGGCAGTG GGAAAAGCAA GGGGAAGACC CAGCCTGGTC
10801 AACATGGTGA AACCCGTCCT CTACTAAAAA TACAAAAATT AGCTGGGTGT
10851 GGTAGAGCAG GCCTGTAGTC CCAGCTAACT TGGGAGCCTG AGGCAGGAGA
10901 ATCACTTTAA CACAGGAGGT GGAGGTTGCA GTGAGCCGAG ATCGTACCAC
10951 TGTA CTCCAG CCTGGGTGAC AGAGTGAGAC CCTGTCTCAA AAAAAAAAAA
11001 AAAAAAAAAA AAAAAGTGGG GAAGGGGAAC ACTGATCCTG ATTATCTACT
11051 CCATATACTT ACTATGTACC TACTACCTAC ACAGGGACGG TGGGCTTTAC
11101 GCATGCCATT TATTCACTGT ATAGAGATCT CAGCATCACA TAGGAGCAGG
11151 GAGTCTTGAA GTTGGCCTTG CTGGCATTTG AGAAGTTTCT TGGTGTATTC
11201 TTCAGGTTCA CGCTCCAGA CAAGTGTAAG TGCTATTGAA TGCTGACTAT
11251 GTTCCAGGAA CTAAACCAGA TGCTAGAAGA CACGCAGTAA ACAGTACAGA
11301 TGCAGGTGCA CATGTGAGGG TCCACACAAG ACCTGAGAGA AGGGAGGGGT
11351 CTTGCTGCAG TTCCCTTTT GTAACAAAGG AGAGAGTACT GTTGACCTC
11401 TTCCTAGGAA CTGTGAGTTT GACTGAAATG TGTCTGCCA CAGGATCTTT
11451 GCTGCTTCCT CTACCTGATT CTTTGGATCT CCCTGCTGGC ACCTTCTTGT
11501 CATTTAGGTC TCAGCTCAA TGTTACCTCC TTTAAAATGT CTTCTCTGGC
11551 CAGCCAGTCT AAGGTTGCTT GTGCTTGGGG TCTCCTCACT CTCTACTTTA
11601 TCCCGCAGTT GCTTCTTATC ACATATGGCT CTCTGAAATT AGGTATTTCAT
11651 TACTTACATC TGTCTTCCCC ACTAGAATTA AGCTCTGATG ACAAGGATCT
11701 TTCTGTGCTG TTCATAGCTT ATCTTCTAGT ACCTGGCTTA GTTCCTGGCA
11751 CATTGTAAGC ATTCAATAAC AGTTTGAATG AATGAATTAA CAAATGAAGG
11801 AATGAATGAA TGCATTTTCC TAGAGGACTT CTGTTCTTCC CTGAGGGAAG
11851 TTATAGGTCG TATTGGTTTC TTGGGACTGT TTTTGTGTTG TTTGTTTGT
11901 TTTGTTTTTT GAGACAGAGT CTCACTGTAT CCCCCAGGCT GGAGTGCACT
11951 GGCACAATCT TGGCTCACTG CAACTTCCGC CTCCAGGTT CAAGCGATTC
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FIGURE 3D



Docket No.: CL001188
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Title: ISOLATED HUMAN RAS-LIKE PROTEINS...

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12001	TCATGCCTCA	GCCTCCCGAG	TAGCTGGGGA	TTCCAGGAGC	CTGCCACCAC
12051	GACCAGCTAA	TTTTTGTATT	TTTAGTAGAG	ACAAGGTTTC	ACCATGTTGG
12101	CCAGGTGGT	CTTGAAGTCC	TGACCTCAGG	TGACCTGCCT	GCCTCTGCCT
12151	CCCAAAGTGC	TGGGATTACA	GGCATGAGCC	ACCACGCCCG	GCCTGTTTTT
12201	TTTTTTTTTT	TAAGACAGAG	TCTTGCACTG	TCTCCAGAC	TGGAGTGCAG
12251	TGGTGTGATC	TCAGCTCATT	GCAGCCTCAA	CCTCCTGGCC	TCAGGTCCAG
12301	GTGATCCTCT	TACCTCAGTC	TTCTGAGTAA	CTGGGCCCAC	TGGTATATAC
12351	CACCACACCT	GGCTAATTTT	TAAATTTTTT	GCAGAGACAT	GGTCTCACTA
12401	TGTTGCCCTG	ACTGATCTTG	AACTCCTTGG	GTTCAAGTGA	TCCTCACACC
12451	TTGGCTTCCC	AAAGTGCTGG	GTTTACAGGT	GTGAGCCACC	ATGCCTGGGC
12501	TTGAGACTGT	TAAGATGATG	AGGCTGGAGG	GAGTGGATGG	CCTCACTGCT
12551	TGAGCCCTAG	AGATTCTTTA	CTCCAGAGTG	CCCTGGCTGC	AGAGGTGGCC
12601	CTGGAGGGTG	ACTCCAGCAA	CCTGGCTGAG	CTGATGGGCA	TCATCTGATA
12651	CCAGCTCTGA	CCCTGAATAA	TAGGCAACAT	GGACCTTAGT	CTAAAGCACT
12701	GACCCCTCAT	CTCTGCATAT	ACCAAAGAAG	ATGAGATTTG	GGTGAGGACA
12751	CAGCCAAACC	ATATCAGCTC	CCGGGATCCC	TGTGTGAATG	GGGTCTTTTT
12801	TGGTGTTTGA	GGGCTGCACA	GGGTGACCTC	TTTAGAGGTG	ACCTCCTGCC
12851	ACAACCCACA	GGAGGTGCAC	ATGGCCCACA	CATGCTGGTT	TCCTGCAGTG
12901	GGAGGCGGTG	GGGCACTCCT	GGGACCTGTG	CTTGTTAACT	GGAGCTGGCC
12951	TGGCCCTGGG	GATTGGGTGT	CTGCCCTGGG	TTTCAGGTGT	ATTAGGTTGT
13001	TCCTCGTTGT	GGAGTCTCAT	TACTAATGAA	AAGTTCAGGT	CGCACTGCTG
13051	GTCTTTTGGG	CTGTGGTTGA	TCCTGGTGAT	AACATTGGGC	ACCCAGAGGC
13101	AGCCCTGTTT	CCACTGAAGC	ATGCGGAGCT	TGGCTGGCAG	GCAGGCAAGC
13151	TGGCAGCTGC	CCTTAACCCA	TGAGGTGCTG	GCCCCGTAGT	AGGCACACCC
13201	TACCTGTGCC	AGAATTGAGG	TTGTAGCCAG	ACTCCAGGAG	CCATCTGGGC
13251	CCCACAGGGG	GCGGCATTTT	CTCTTTTGTG	TGAAACATTC	CAGCCAAAGT
13301	CTGGCTTGGG	CTTCATCTCT	CTGTCCCACT	CTCCTTCTCT	TCCCCAACAT
13351	AAGCCTCCTT	CTACATCCTA	GAGCTCTTTC	CATTCCCCCT	CCTGCAGCTC
13401	TGGGCTCGCT	AATCTCATGC	TTCCCTAAGG	GAGCTTGACG	GCTGCTTCTG
13451	CTAACATTTA	ATAAAGTTCT	GCGTGCCAGA	CCCTGTGTTA	TGGGTTTTAC
13501	ACCTTATCTC	ACAATCTTAA	AAAAAAATTT	CTCTGAGAAT	CCTCTGTCAC
13551	CCCCACTTTA	CAGGTGAGGA	AACTGAGGCA	AAGATAGGCT	AACTGGCTTC
13601	CCCAACACCA	TGCAGGTAAT	TAGTGATAAA	GGCAGGGTTG	GAACCAAACCT
13651	TGACCTCCCA	ATTGTGCTCT	TAATGGCCAG	GACACTCTGT	GTCTTGAGCC
13701	ACACTTCCTC	CATGTTTTCT	AGGGCTTTCT	AGGGAGGCAG	ACAGTGATGG
13751	GAAGGGGTGT	TCTTTAGTGT	GGATGTGCCC	TGCCTGCTCC	TTTCTGTAA
13801	CGTCACAGCA	CCTCCACTGC	TGTACTGGGG	AGGCACCAAG	TTTTTCCCTG
13851	TTTGCCCACT	CAAGGCGAGC	TAGCTTAGGA	GTCACGTGAG	TGCTGGGTGT
13901	CTCGCCTGCT	GCATCCCTCT	ATCCTGCCCC	TGCCCCCGGT	GCCCCAGGGA
13951	GGGCCCTGCC	TGTCTTCCCA	GTTCTCCAAC	AGCAGCGCTG	TCCCAGCACC
14001	CTCGGGCTCC	AGTTGTGGCC	TGGCAGCTGC	TGGGGCAGAC	ACCATACAGA
14051	CAGAGTCACA	GCAGGAAGAG	GATGGGGCCC	AGGGCTGCTG	CCTCAGGCCA
14101	TGGCTGCATG	GCACCATCAG	TTGATTGAGG	AGCTTTTCTT	GCCAATGTCT
14151	GAGGCATCAG	GTGGCAGGAC	ACGTCTCCCT	GCTCTTAAGC	CTCAGGCATG
14201	CAGCCCTTCT	TATGCTCTCT	GGGGTGAGGG	GGAGATCCCC	CTCATGGAAT
14251	TGCTTTTTTT	TTTTTTTTTT	TTTTTTTGAG	ACAGGGTCTT	GCTCTGTCAC
14301	TCAGGCTGGA	GTGCAGCCTC	AACCTCCCAG	ACTCAAGTGA	TCCTCCTGCC
14351	TCAGCCTCCC	GAGTAGCTGG	GACCACAGGT	GGACACCATC	ACACCTGGGT
14401	TTTTTTGTCT	TTTGTTTTTT	GTTTTCTAGA	GATGGGGTCT	CACTTTCTTG
14451	CTCAGTCTGG	TCTCGAACTC	CTGGGCGCAA	GCAGTCTCTC	CACCTCGTCT
14501	TCCCAAAGTG	TTTGGATTAC	AGGTGTGAGC	CACTGTGCTT	GGCCTTTTTA
14551	TTTATTTAGA	ATTTGTTTTG	GAATTGCTTC	TTTATGCCTG	GCATATGCTT
14601	GGCACTATGT	GGCAGAGATT	TTAAAAACGA	GCAAACAAAA	CAAATGCTTT
14651	GTCAACCACA	AAATGTATTC	TCTGCCCCCT	AGGTCTTTTT	TGTGTAGTTG
14701	AGGCTAGAAG	ACAAAAATAG	GGGGCAGTAA	GGAGCAGGGA	GCGATGTTTT
14751	AGGAGGTCTT	CCTTCCAGCC	CCCTTGTTGA	AGCATCTGGC	TCCTAGCTTT
14801	GGGGGAGCCA	TTAGGCAGCA	GTGGCCAAATC	CTGAGGCACT	CTCAGGTGTC
14851	ACTAAGAAAA	GGGGCATGTG	CTCTATGGAT	ACCCATGGGC	TGAACCTGGA
14901	GTCTGGTCTG	GACCCATGGC	TGTGCTAGGA	TCCACCGTCC	CCAGCCCCAA
14951	CTGCAGTCAG	CATGTTTCATC	ATCCTTAGGC	CTCTCCGCTT	CTTTCTGCAT

FIGURE 3E



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15001	GTTTGTCTGC	CTCATGCCCT	GCTCATTACC	AACTGGTCAG	TCCCCACTGC
15051	CCTGCCTGGA	GTGAGCTGGT	TTGATTGGCT	TAGCTAAGCT	CCCTTGCCCTC
15101	TGCTGGCCAG	GTCACCTGT	GGGTACCAG	CAAACCTGTT	GATGGTCCAG
15151	TCTGAACCTG	CTTCTCCACA	AAGAACATGT	TGCACCCAGC	CCTGCTTCTC
15201	TGAGCAGAGG	TTTGGGGCTG	AGCTGTTCTA	GCCAGAAAGG	GACACAGGGT
15251	GTGGCAGGCA	CCATGATGGG	CATATCTAAT	GTGCCGGGAA	AAACAATGAG
15301	CTGCTCTCCG	TGCTTTGGGC	ACCTGGTTGG	GAGAGGGCCC	ATCTGTCTGA
15351	CTTTCTCCTC	CTGGGGCTCT	CAGCGTCTCC	GAGAACCTCT	GCCAGAGCTG
15401	TGTAGAAGTG	GTTTGCTTGT	TTCTTAACAC	TTCTGTGCCC	TATTTCTTTC
15451	TGTACCCAAG	AAAGGAAGTA	GACTGTTTTG	TAGGGACACT	GTCCGGGTGA
15501	TGAATCTGGA	CTTACTGGAA	TCATGAACCA	TGCCAAGGAG	GAAGGAGAAA
15551	ATAGGCTATG	GTGGGTGTCT	TAGTTAGGGC	TGGCTGCTGT	AACAAAATGC
15601	CTTTAGCTGA	GTAATTAA	GCAAGAGAAA	TGTATTGCTC	AGAGTTGGG
15651	AGGCTGGGAA	GTCCAAGATC	AGGGTGCCAG	CAGATTCAGT	GTCTGGTGAA
15701	GGCTGATGCT	CTGTGACAAA	GGTGGCACCT	TCTAGTCCA	TCCTCACATG
15751	GCAGAAGAGG	GAACAAGCTC	CCTCAGACCT	CTTTTCTAAG	GGCGTTAGTC
15801	CCATGCATGA	GGGCTCTAAC	ATCACGACTG	AGTCACCTCC	CAAAGCCCTC
15851	ACCTCCCACC	AGCACTGCAC	TGGGGATTAA	GTTTCAATAT	GGGAATTTTG
15901	GAGGAACACA	GACCTTCAGA	CCACAGCAGC	GGGCTTCTCC	TCATGTGCCC
15951	CCTGCCTCAC	TTCTAGATGC	CGCATAATGT	CAGTGAACC	CCGTCTCTAC
16001	TAAAAATACA	AAAAATTAGC	TGGGTGTGGT	GGCACGTGCC	TGTAATCCCA
16051	GCTACTTGGG	AGGCTGAGGC	AGGAGAATCG	CTTGAACCCA	GGAGGCAGAG
16101	GTTGCAGTGA	CCTGAGATCG	TGCCACTGCA	CTCCAGCCTG	GGCGACAGAG
16151	GAAGACTCCG	TCAAGAAAAA	AGAGAAAAGG	CATCAGGTAT	GCCAGGGTGT
16201	GCGGAAAAAG	GCATCGGGTA	TGCCAGGGCG	TGTGGGAAAA	GGCATCGGGT
16251	ATGCCAGGGT	GTGTGGGAAA	AGGCATCGGG	TATGCCAGGG	CATGTGGGAA
16301	AAGGTGGTAA	GATTCTCTAG	CCTCCCAGGG	TTGGGAAGCC	TCTGGCCGAG
16351	TGAAGCATAC	CCTGGGTGGG	TTTTAAGACA	CCAGCTTTC	AGTCCAGCTC
16401	AGCTGTGGGA	TGTGGGAACA	TGAGTCAGTG	GGAACATGAG	AATTGGCTTC
16451	CCTGTGGCTC	ACAATAATAC	CTACTCCTGC	CTACTTCATG	GGACCCGCAT
16501	AAGAGCTGAG	GGATTCCATA	GCTCAGGGGT	ATGCTGTAAA	GACAAGCACT
16551	ATGCACCTGG	GTGTGGTTCT	GAAACTTCT	TGTGCAGAAG	AGTGAGTAGG
16601	GCTGGGCGAG	TCGTGAGAAT	GTGCATTCT	CACACACCTC	TGATGCTGCT
16651	GATGCTCTAG	TCCCTTGCT	GGCAAGGGTA	CCTGGTTAGT	AGGGGCCAGG
16701	ACTCTGTAAT	GCCTTCCACT	TCAGGGTTCT	CTGGGCTGGT	TTTCCTGACT
16751	CCCCAGGAAG	CCTTTATTCA	GCAGAGGGAA	GGTAGGAGTG	AGAGGACTAC
16801	GCTGTCTAGT	CTTCACATAC	ATCGTTTAAT	TTATCCCAGC	ACAGCCCTTA
16851	GGAGGGAAGC	AGTATTCTCC	TTCTACACTT	AAGAAAATCG	GCCTGGTGCG
16901	GAGGCTCATG	CCTATAATCC	CAGCACTGTG	GGAAGCTGAG	GCGGGAGGAT
16951	CGCTGGAGCC	CAGGAGTTCA	AGACTAGTCT	AGGCAATACA	GGGAGACCTC
17001	ATCTCTACAA	AAAAAAAAAA	AATTAGCTGG	GCATGGTGGT	GCACACTTGC
17051	AGTCCCAGCT	ACCTACCCAG	AGGCTGAGCT	GGGAGGATTG	CTTGAGTCCT
17101	GGAGGATCGA	GGCTGCAGTG	AGCTATGATT	GCTCCACTAC	ACTCCATCCC
17151	TGGCAACAGA	GTGAGACTCC	ATCCCCAAAA	AAAAAAAAAA	TTGAAGCTAG
17201	GAGAAGTTGA	GACTTGCCCTG	AAGTTACACA	GTAAGTGCCA	GAACCAGGAC
17251	TTGGACCAGG	TCTTTCTGAC	TCCAGGCCAA	TGGATGTTTC	TTCCATGACA
17301	TATATAGCTC	TTGAACTAC	TTCTATCTAA	TATCACCAC	AGTGCTGTTA
17351	AAAATACAGA	TTTCTGGGCC	TCACCCTCAA	ATTATGATTC	AGTAGGTCTA
17401	GGCACGTCAA	GGTCATTGTT	TTTGTCTTTG	TTTTAAGTCA	CCCCAGGTGA
17451	TTCTAAAGCC	GAAGCTCTGC	AAAGCACACC	TTGAGAAACA	GAGAACTCTT
17501	GTGCTCTCGC	TCTCTTGACA	CTTCAGGTGC	AAAACTTTTC	TCCTAATGTC
17551	GTTCTCAAAC	TTACGCATGT	GTGAGAATCA	CTGTGAGAGC	TTATTGAAAC
17601	TGATTGCGGG	ACCCCATACC	TAGAGGGCCT	GATTCTATAG	GTCTGAGGTA
17651	AGGCCCAAGA	ATTTGCATAT	TTGCATTTTC	TTTTCTTTTC	CTTTCTTTTC
17701	TTTTTTTTTT	TTTTTGAGAT	GAAGTCTCAC	CCTGTCGCCC	AGACTGGAGT
17751	GCAGTGGCAT	GATCTCAGCT	CACTGCAGCC	TCTGCCTCCT	GGGTAAAGC
17801	GATTCTCCCC	ACACCCAGCA	CCCGCTCCTG	AGTAGCTGGG	ATTACAGGTG
17851	CCCGCCACCA	TGACTAGCTA	ACGTTTGTAT	TTTTAGTAGA	GACGGGGGTT
17901	TCACCATGTT	GGCCAGGCTG	GTCTCAAAC	CCTGACCTCA	GGTGATCCAC
17951	TCACCTCAGC	CTCCCAAGGT	CTTGGGATTA	CTGGTGTGAG	CCACCGCGTG

FIGURE 3F



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18001	CGGCCAGAAT	TTGCATTTCT	AACAAGTCCC	AGGTGATGCT	GATGCTGTGG
18051	GTCCAGGGAC	ACACTTTGAG	AACAGCTTGT	TACTCAGGCG	ATATGTGGAC
18101	AGTAGCGTCA	TCTTCACCTG	GGAGCTTCCT	GCAGCATCTC	AGGCCTTGCC
18151	CTACACCTAC	CAGATCAGAA	TCTGCATTTT	AACTCAATCC	CCGCGTGATT
18201	CTCATGCACC	TGGAAGTTTG	AGAAATATGA	CCTTAGAGGA	GCCGGAATGT
18251	GAAACCACTG	GAGGCAGAGA	TAGATGGAGA	ATATCTCTTC	TTCTCACGGA
18301	TACTAAAGAT	GCAACAAAAA	GGGCTGACTC	TCTGGGTGTG	CACCCAGGTG
18351	GGGCTGATGA	CCGAAAAGAG	GCCAGATGTG	GACAGAGGAC	TCTTCCCTGA
18401	GGGAAGGCAG	AGAGAACTTA	GGAAAATCTG	AAGAAAGGAG	GTGGCTTCAG
18451	AGGAAAGGCA	TTCATCTGGG	CCATAAAACA	GTGGAGAAGG	TATCCTGCTG
18501	AGAGCACAGG	GGTGGGGAGG	GGGTGCCCTG	GAGCTGAAGT	CTTCAGTGGG
18551	GGGACAGTGA	TAGGTGAACA	CACATGTGAA	TAAACAGTTT	GCTAAGCAGC
18601	TGCGAGGGCT	GGCCAAGGTG	AGAAAGCATC	CGTCTGCAGA	GGCCTCAATA
18651	AGGCCAGTGT	GTTGACTTTG	TCCTGCAGTG	CTCAGCAGTG	GAAAAAACCA
18701	ACAGCCACGC	AGGGAGAGGG	AAGGAGCCAC	GATGGGCACG	GGTTACTGGG
18751	GCCAGGGCTT	GACTGGTAGG	TGGACACAGC	TGAAGGCCCA	GGTTGTGTGG
18801	GAACAGAGCG	CAGAAGCAAT	AGATTCCCTC	TGAAGATCCT	TGGGCTGTTA
18851	ACCTTTTFTA	AATTTAAGAG	AGGTTGTGTG	GGCGGGGAGG	GAGGAAGGAA
18901	AATCCTTTCA	AAGACATAGA	CTTACTCTGT	TTCTTCCATC	ATATGTGAAT
18951	GCATATGAAT	AGCCAAAAGG	TGAATAAAAC	ACATGTTCCC	AGGTGGCCAG
19001	TGAGACCTAG	GTTGCAAGAT	GGTGGGGTGT	GTGTGAGGCC	GGGGAGTGCT
19051	GCGAGCCCGC	GAATTCCTCA	GCCTTAGTCC	CCCGCCACAT	AGCTAAGAAG
19101	TGAGGGAGGA	GGTGAGAAGG	AGTCACTGCC	CAGCCTCACT	TCCGGTGGAG
19151	TACCCTGTCT	CCTGTGTCAGT	TCTGTCTCTG	GGGACAGTTG	CCTGCTTTCA
19201	CCTCTCCCTC	CATCCCCTCT	TCTCTCACAG	GGAAAAATTC	ACCTTAATAT
19251	TGGAAGTTCC	TCTCCTAGCA	AAGTCCTTCT	CAGGCACCCA	CAGGCAAAAA
19301	GGAACTAAG	CAGAGTTAGG	GCTTCCAGGC	CTAGCCAACT	ACACGACTCT
19351	CCTCTTGCTT	CCCTAAGAAC	CAGCGCAAGG	GGCAGCGTGG	GTTCCAGCAT
19401	AGATGGACCT	GTGTTGGAAT	CTCTGCACGT	GCTGTGCTGA	CCCTGGCTAG
19451	CCATTGACCT	CTCTGAGCCC	TTGTTTCCTT	TCCACTAGGC	TCTCTGAGGG
19501	CAGGGGCCAT	GTCTTTTTC	CTGCTCTGTC	TGCACTGAGC	ACTGTGCAGG
19551	GCACATAGGA	AGTTCCCAT	AATGTTTGTG	GGATAAAGGA	AATAAACCTT
19601	TCTCTCTTCC	TGTCCCCCTT	GTGATGGCTT	TGCACAAGGC	ACTGTCTTGG
19651	GCCAGGTTTG	CTAGGCTAGT	GTGAGGATAA	ACCAGGTATA	TTACAAATTG
19701	GAGAAAATTT	CTCGTTCTTC	TTGGAAGAAG	GTGCTGTATC	ATGAAACAAG
19751	AATGTCTTGA	TTCCCTTCTA	TGCCAGGTAC	TGGGGAGAAA	CAGGTGCCTG
19801	ATAACCGTTG	ATCCAGGCAG	AAATAAGCAT	ACTCCTGCTT	CCCAAGGCCT
19851	GATGCTTCTC	TCCTTCCCTC	CTTCTCTCCT	CCTTCTCTCT	ACTCTTCTCT
19901	TGCACACATG	GAAGAATGGC	TGCCAGGCAT	TGCCCATTTG	GAAAAGTACA
19951	GCTCAATGGA	TATGAATCAG	CTTGGGCAGG	CGAGAAATGA	TTACCGTCTG
20001	ACCAAATCGA	TTTAGTTCAG	GTTGCCCGTT	CTGCATCTTT	TTTCCCTTGT
20051	AATTAAATGA	TGATTGGTCT	TGATGGTGGG	AAGGAAGAGA	CAGAATTAA
20101	TTTGTTTGCC	TTTGTTAGAAA	GCTGGGGACA	GCACAGATAA	GGGAAGATGT
20151	CTCCCATTTG	GCAAATAACT	GATGCGGAGG	TGGAGTGGCA	GTGGTGATGG
20201	GGATGCTGGT	GCACTCAGGC	CTTCTGGGCC	GGGCAGTGCA	GCTGGTGGCA
20251	GACGGTTCGG	AACTCTACCA	TGTTCCCATC	TGAAAACGTG	GGCTGATCAT
20301	GCCCACTCCT	GACCTTGCTC	CAGGGAGTAC	ACAAAGACGT	AAGCTTAATT
20351	AACCCACCAG	ACGTAGCTCT	TGAATCCCTG	GGCATAGTGC	CTGGGTATAG
20401	TTAGAGTTGG	GGAGAGGCAT	GGTCAGCAAA	ACAACCTCCC	TCATCTCTCT
20451	GTTGTCACTC	AGAGTCAAGC	TGGCTGCTGC	TGGTGGTGCT	GACTTCTCTT
20501	GCTGCAGATT	TCTCCAATAT	GTTTCTGCCC	TGCACGCATT	TGCCAAATCC
20551	CTTCGGTTTC	TTGTGCTCG	TGGCAGCTTA	GCTCCTCCAG	CCCTTGATG
20601	AAGAAGCGTG	GGAACTCTTT	GCTTCTCTTC	CCTCCCCGAG	TGACATGCCA
20651	TGCCATGCCA	CTGCCTCTTC	ATCTGGTCTC	ATGACAGTCA	CTCATAAGCA
20701	CCCGCATGTA	CCCGGCCCTG	CACTAGCTCA	TGACAGCTGC	AGTCAATTGG
20751	GCCAGGTGCT	GTATCTCATC	CGGCCTCCTC	AGCAACCCTC	TGAGATACTG
20801	GTAATGTCCC	TGATGAAGAT	ATTTACTGAG	GCAGAAATGG	ACGCTCAGTG
20851	AAGCAAGGTG	CCTGATGTTA	TAGCAATGAG	CTATGAGTGG	CCAGAGGGAG
20901	GAGATAAGCT	CAGGCCTGAC	ACCAAAGCCC	ATGCTCCTTC	TAGTCAACCA
20951	CAGTGCCCTC	TATGGTGAAT	GAGTGAGTCA	GCAACCAGAA	CGCATGAGGC

FIGURE 3G



Docket No.: CL001188
Serial No.: 09/817,198
Inventors: YE, Jane et al.
Title: ISOLATED HUMAN RAS-LIKE PROTEINS...

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```
21001 CTTCTTTTGTG GTGAGCCTTG GCTGGGTGCT GAGGCTTCAG GTACAATCAT
21051 GGGTTGGAAG AGCCCTCCTC TCTCTCCACA GTCTGGCACT ATGACCCCTT
21101 CTGGTTATTA ACAAGGCAAA GAGAGAGAGG GAAGAAAGCA GGCAAATAAT
21151 GTGGGTGCTT ATTCTTAGAG ATTAGAATTT CAGGAAGGAT AAACACAGCG
21201 TTCTCTCCAG AAGTATAAAT AGGAAGACTT CACACATGAC TAGAACGAGA
21251 CATGTTTTAA GTCTGTCTGAG TAAGGCAGTG ATGAAGTAGA TTTCCCCAGA
21301 TTCACTCTCC CTCTCTGGG TCCCCCAGGG CCTTTACTTG TGGCAACTTT
21351 CAGCTCAGGG AGGGAGGAAA GCCCCTTTCA AAGCTTCAGA TACTTCCTTA
21401 AGGTCAGTTT CTGCTTAAAG AAGGCCTTTA CATTACTTCA TCCCTTTGCC
21451 AAATTAAACT GAAAGGAAAC CTTTCAAGTG TGATTGCTG GCCCTTTTCT
21501 GTTCATTTCT CGTGGGTACG CTTTCTAACT TTCTTTCTTT CTTCCTTTCT
21551 TCAGGTGTTG ACTTTAAGAT GAAGACCATA GAGGTAGACG GCATCAAAGT
21601 GCGGATACG GTCTGGTGAG CTGGGGAGGA GGAGGAGGCA GATGTAGGAG
21651 AAGAGGACTT CTGGCTGCTC CTTAGCTGCC CTTGCCATGT GTAAAATTCC
21701 TAGGCTTCAC CTGGGATAAC TGGCCACCTC TCTGATGGAT GGAAGCGAAG
21751 TCTCAGAAGC CCATCTCTTC CTATAAGCCT TAATCTCCAA CCTCTAAGAA
21801 ACTTTAGGGG ATTGACTACA AGCACCAAAG GGCAGGAATT AGAAGGAAGT
21851 GGCACACTAA CCATTGTGAA TTTATCTCAG GATTAGGCTT TGCCCTTGGG
21901 CTGTGCTAAG CATGTTAAG ATTGGAAGGA AGGAGGCTAC ACCCCCATC
21951 ATTTAGGGCG AGACCCTGAG AGAGTTCCTC AGGATAGCAT GATGAAGTTT
22001 CCACAGTAGC AGAGGGTGCT GCTGTGGCTC TCTGCCTGAG GTCTTGGAAG
22051 CACTGCCTTT GCCAGGTTT AGAGCTCCCT CTCAATTCCA CAGCAGTATG
22101 GGCAGTGCCT TCAGAGGTCC CATAGGACT AGGGGTGTAG CAGCATCCCC
22151 TGCCAACTCC CATCCAACCA AATCTGGCCA CAGTGGCCAG ATTCCAGAGA
22201 GCTGTCCAAG GCCTGTCTG GCTGTGGCTT CTGGTTCTG CCAGGAGGGC
22251 AGTTGGCAGG AGGGGCCAAG GCCCTGCAGG CCTGGTCAGC ACCAGCACAG
22301 ATGACCAGGC CTCTGACTGC AGATCCCTGT GGGGATCCAA GCATCCCTGG
22351 TTTTTCACCC TTTAGCTCCC CAGTTTTTCC TACAAGGGGA CAGCTCTGCT
22401 CTTCCCTCC CCGTCTGTTC CCATGGTCCC TGCTCCTCTG AGGGACTGGC
22451 TTTCTCCTGC AGGGACACTG CAGGGCAGGA GAGATACCAG ACCATCACAA
22501 AGCAGTACTA TCGGCGGGCC CAGGTAAGCC ACCACATTGG GGGTTTCAAA
22551 GTGGGAAGCT GCCACCCACA CTCCAGCTC TGGGTATTG AGATGTCTGT
22601 GCCACGGATC CCCTAAATAC AGTTCGCCTG CTTGGAGGAG CGCAGGGCGT
22651 CTTTCAGCTG TTTACTGATC ATTTGTCCGT CCATTGTTCA TGGCCCACTC
22701 ACTGCAGGCA GGCCCTGCC CTCACCCCTG ACTTCCACCC TCCATCCTGG
22751 GTCAAAGATC CAGGTCAAAG CATGTGGTGT CTTCTCTCTG TAGAGAGTTC
22801 TGTGATGGGC CTGGGAGGCG GCAGTGGTGG GGTCTGAGAG AAGAGATATT
22851 TCTGGATGCT GAGCAGGGAG AATGGGAGAG TGGGACCCAA CCTTTAAGTT
22901 TCCACGGCCC CTTCTGGCCC CATGACTGCA CTCTCTCTGT GCATATCACA
22951 TCTCTCTATT TCTCTCTCTC TCAGGGGATA TTTTGTGCT ATGACATTAG
23001 CAGCGAGCGC TCTTACCAGC ACATCATGAA GTGGGTGAGT GACGTGGATG
23051 AGGTAGGAGA TGCCACCTCA CTGCCGGGGT GTGGAGAGGG TGCCTCACCG
23101 GGAAGGCAA GCGAGGGCC AGATGGGAAG GCAAATGCTT CCAGGAAGCT
23151 TTGCCTTCCA CAGCCCTGGA TGAAGACCTC TGGGTGAGTA AGACATGGGG
23201 AAGAAACCGA AGCTGCCATG CCCTCACTCT CTATACCCTG CCAGGCCTCC
23251 ACGGCTGTGT CTTTCCCGGA AATGAATTAG TTCCAAGTCT TCCCTGTGAG
23301 CAGCTTCTTT CCTGAAATCT TGGGACCAGG TGGAGTTGCA AGATTGGGAT
23351 CTAGTCTGG CTCTGCACAA TAGCTGTGGA GCCTTGGGAA GCCATTTGAA
23401 TCCTCTGGGT CCCAGTTCC TGTAGAAATGA GGGCTGGACT TACATCCAAT
23451 GTCCTTTCCA GCTCTGATAC CAGTGGTCTA ACCCAAGGAA GCACAGTCT
23501 TAGCCAGAGT GTCTTCTACC CTAAGCTCTC CCCGTGATAC CCTTGAGGTC
23551 AGCCATGGCA CTTGGGGGAG CCTGGCACCT GCATCCAGTC GGCCACCCT
23601 GTCCCTAGGG CTCTGGAATT GGTGGTGGGC TGGAGGAGT GCAGACTCTG
23651 TAGGGAATAT TGGGGGGGCA GGCAGCACTC ACTGGCTGTT CTGCCCATCC
23701 TTTGTCCCTA GTACGCACCA GAAGGCGTCC AGAAGATCCT TATTGGGAAT
23751 AAGGCTGATG AGGAGCAGAA ACGGCAGGTG GGAAGAGAGC AAGGGCAGCA
23801 GGTAAGTGGA GGGAAAAGGC AAGTCCACCC CAGGTCTCTCT GCTGGGCCCTC
23851 CAGGGCCAGT CCTGAGCGTG GGGACCTAGG GGTGTGTTCC CCAGTGGCAG
23901 GTCCTCCAC ACGTCCACAG CACCCCAAGG CCCTGGGGGA GTGGCCATCC
23951 TCGGAAGGCT TGTTGTCTGG GTTTCAGGAC AGAAGCCAG AGATTGGGG
```

FIGURE 3H



Docket No.: CL001188
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Inventors: YE, Jane et al.
Title: ISOLATED HUMAN RAS-LIKE PROTEINS...

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24001 TCCATCCAGA AACAAAGACG TCATAGGCAG CAACTCTCCC AAGTCCAGGT
24051 CCCCAAATGC AGGATTGCCC TCTGCTTAAG AGATCATCCC CGTGTTAGTA
24101 ATGAAGGACT TCAAGTTGTC AACCTCTTCT CTGACAGCAT CCAGGCCTAG
24151 CTGCCATGTT ACGGTCGAGA AATGATCTCC CATCCCACCC AACACTCCCC
24201 CACTCCTGTC CTTCTTACCC AGGAAAGAGC CAGGGAGGCA AATGAGGAGA
24251 CAAAGAGCCA CAGCTGGAGA AGCCATGGGG GCAGAAAGGG TAGGAGGATG
24301 ACGCTGAGGG AATGTCCAAG CATGCAGGGA GACCATCCTC CCAGAGAGCA
24351 GAAAGAAATA TTGGTTATTT TTTTTTCTT TCTTTCTTTT TTTTTTTTTT
24401 TTTGAGATGG AGTCTCGCTC TGTCACCCAG GCTAGAGTGC AGTGGCGCCA
24451 TCTCGGCTCA CTGCAACCTC TGCCTCCTGA GTTCAAGCAA TTCTTCTGCC
24501 TCAGCCTCCC AAGTAGCTGA GATTACAGGT GCATGCCACC ACGCCTGGCT
24551 AATTTTCTTG TATTTTTAGT AGAGATGGGG TTTTGCCATA TTGGCCAGGC
24601 CGGTCTCGAA CAGCTAACCT CAGGTGATCC ACCTGCCTCA GTCTCCCAAA
24651 GTGCTGGGAT TACAGGCGTG AGCCACTGTG CCCAGCCAAG ATTGGTATTT
24701 CTGAGATAAG TTATCCACTC AGTCCGTGGA CCTCAAGAGT TTTCTCTCTC
24751 CTTTTTCAGTC AATAGCGTTC CATTAGTACT TAAAAAGAAA TTGATTGTTT
24801 GGTATAAAAT ATAAGACATG GTCATTGACC AATTTGAAAAG TAGAGGCAAA
24851 GCCTACTAGG ATAGTATTTA TTGAGCACTC TATGTGTGGC ACTGTGCTAA
24901 GGCAAGCGCT TTTAAGTGCA CGACCCCACT GAATCATCCC ACAACCATGG
24951 ATGGGAGACA CACTCAGTCT CCTTTAACAG AAGATAAAGC TGGGGCTTAC
25001 AGAGAATGTA CAACTTGTC CAAAGTCAAC AGCTAGCCAT CAGTGGCAGT
25051 GCTGCTATTC AGGTCTGGGA CTGTGGGACT CCAGAGCCCA TGTTTTTTTAC
25101 GAGGATGCCA TACTGCCACA ATGGATGGTG TCTTTATCTC CTGATATATG
25151 ATTGTGTGTT GGGAGGCGTG GGGTGGCAGC TGGAAGAAATG GAGAGGCATA
25201 TTTGTGGAGG ATCTTCCCCC ATTCTCTGCT ACCCTCTCTT GGAGCTCCCA
25251 GTCCCATCTG AGAAATTATC TACTCTGAGA AATCGTCACA ACACAGCATG
25301 GTTGTGAGTG CAGTGGCAGA AGCCTGTGCC TGGTTGTATG GGCCCCTCCC
25351 CTGCCTTACT GACTCTCTTT CAGAAATGTC CTTCTCTTGC AGCTGGCGAA
25401 GGAGTATGGC ATGGACTTCT ATGAAACAAG TGCTGCACC AACCTCAACA
25451 TTAAAGAGGT GAGAGCCCTG GTGACCAGGC GCCCGCTCTC TCGGGCTGAG
25501 TCCAGCAGAG GTGGGAGGAG GAGCCATAAG ATGGACCTTA TCCCTCAGGC
25551 CGCTGCAGGG TTGCCAGGGG AGAGGAGGAG AACTTGACT AACCTGTGCC
25601 CTTTGGTTTC CAGTCATTCA CGCGTCTGAC AGAGCTGGTG CTGCAGGCCC
25651 ATAGGAAGGA GCTGGAAGGC CTCCGGATGC GTGCCAGCAA TGAGTTGGCA
25701 CTGGCAGAGC TGGAGGAGGA GGAGGGCAAA CCCGAGGGCC CAGCGAACTC
25751 TTCGAAAACC TGCTGGTGCT GAGTCCTGTG TGGGGCACCC CACACGACAC
25801 CCCTCTTCCC TCAGGAGGCC CGTGGGCAGA CAGGGGAGCC GGGGCTTTGC
25851 CCTGCTGCTG TCCTCTCGTG TGATGACCCT ATTGAGTATC AGTAGCCACT
25901 ACTCCCCCTG CCTGGCCCTG AGAGCGGCTG TGCTGTCATC TCAAGCAGCC
25951 CCTGTCCCCA GCGGCTCCAC CCTGGAGTGG TCTTCTTCAG CCTGTTTCCC
26001 CAGCCACAGG CCTGCTACGA CCCCCACGAT GTGCCGCAAG CACTGTCTCA
26051 CCATCCCGCA CCCACCAGAC AACAGCCAGG GCTGGAGTCC AGGCCACTTT
26101 CAGCTGCTCC TTTCTCCGTG CATCGTGTCT CTTCTCTGCT TTTTCTCTCT
26151 TCCCCCACTT CTCTTTCTCT GACCCCTCCC CTCCGGTGCG TTTCGTATCA
26201 AAGCTCCTCA AACCCCGTCC CCCGTGTGTC CTGCTGTGTG CAGCTCGCTC
26251 TTTCTTCTCT TCCTAAGCTA TCCAAGGGGA TGGACCCAGG CTCGTGGGGA
26301 GGTTCCACCC TTGGATCCAG GAAGAACCCT CCACCCTGCC TCGTGGGTGG
26351 GCCAAAGGCT ACAGGGTGCT TCTTCTCTT CCCCCACCCC CACTGTCCCT
26401 CATGTGCCAT GGGCCTGCCT CCCAGTGAC CTGCGAAAGT GGAGCATCGA
26451 GGTAGGAGGG AAACGGCAAC CAGGGAGTCC TCGAGCCTGG GGCTGCCCTA
26501 CCTCTACCCA TTCCCCGACC AGAGCTTTGC CTTGCTTGG CTGCCCCGCT
26551 GCCTCTTTGG GGAAGTGAGC TCAGAGGCAG GTGCTTCAGA GAAGGAAACA
26601 AAATGAGGGG TGGCAGGAT AAAAAAGTAC CTCCATTCTC TACCTCCCAT
26651 GCAGCATGAA CACAATTCT CTCCACCTGG CTCCCAAATT TAAAGATGTG
26701 GACCAAGGCC TGTGGGTACT CCAGGGGCAA GGAGAGCCCT GGGGTCAGTG
26751 ACACTGTGAG GCCAACCATG CACTCCACAA AGGGGAGCAT TTGGAATGA
26801 AGGACTAGCT CCTATGTATC AGGTAAAGAG CAAGGGAGAG CTGGCCAGGG
26851 ACAGCAGTTT GCACAGCAGA GGGGAATGTA GCAACAGCAG GGCCTCCTAG
26901 GCCCCATCTT CCATTTCTTA GGTAAGAAGA GCATTTCTCT AGACTCCAG
26951 GCGGAGGACT GAGCCTAGCC TTCAGCAACC AAGGTTCTCC TGGGACCCAA

FIGURE 31



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Serial No.: 09/817,198
Inventors: YE, Jane et al.
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```
27001 AGTTTATGGG AGAAGGGCAA AGACTTCATG GGAAGAGAGA AGGAAGGCCC
27051 TGGGTAGAAA CGCTTGGTGC TGTTCTCTTT GGCCTTTAAG ACAAAGCGCT
27101 CATCTTGCCC TCTACCTCCT GATAGGCTTG AGGGTTTGCC AACCACACTG
27151 TGGCTACAGG TGGAGGGAAG AGGACTCCTT CCTCCAGAGT GCTATGTTCA
27201 GGAAGTTTCT TTAACCCCAT ATGGCCCAAG AGTAGCTCGT AGGAGGCCCT
27251 TTAAAGACGG AACAAAGTAAT TTACCAGTTC TACTGGGGTT CCTGCCACCC
27301 GTCCCAAGGT GGGCGAGGCC TAGGAAGAGG GTCATTCTTA AGCCACACAT
27351 TAGCTGCACT GCGTGGCTGC AGCCAAAACA AAGAACTGGG TGTTGAGTAT
27401 TCATCAACTA AGAACC AAAA TCCAGGGCAC TCATATGTGA AGGATAAGAA
27451 CCTCACTTCC TTACTCCTCC AAAAAGAAAGT GGGGAAAGAA CCATCAAACC
27501 TTTCTCTCTG ACTTACCAAA CCAGGAAAAC AGCAGGAGAG GGTGGCTCAG
27551 GACTTAGGGA CAGGGTATAG CTTAGATGGT GGAAAGCAAA GGAGAGCAGG
27601 AAGTTGTAAA TCATGGCTA ATGAGAAAAG GAGACAGCTA ACTCTAGGAT
27651 GAAGCTGTGA CTAGGCTGGA GTTGCTTCCT TGAAGATGGG ACTCCTTGGG
27701 TATCAAGACC TATGCCACAT CACACTGGGG CTAGGGAAGT AGGTGATGCC
27751 AGCCCTCAAG TCTGTCTTCA GCCAGGGACT TGAGAAAGTTA TATTGGGCAG
27801 TGGCTCCAAT CTGTGGACCA GTATTTTCAGC TTTCCCTGAA GATCAGGCAG
27851 GGTGCCATTC ATTGTCTTTC TCTCCTAGCC CCCTCAGGAA AGAAGGACTA
27901 TATTTGTACT GTACCCTAGG GGTTCTGGAA GGGAAAACAT GGAATCAGGA
27951 TTCTATAGAC TGATAGGCCC TATCCACAAG GGCCATGACT GGGAAAAGGT
28001 ATGGGAGCAG AAGGAGAATT GGGATTTTAG GGTGCAGCTA CGCTCACCCCT
28051 AAACTTTTGG TGGCCTGGGG CATGTCTTGA GGCCCAGACT GTTAACCAGG
28101 CTCTGCTGGC CTGTTTACTC GTCACCACCT CTGCACCTGC TGTCTTGAGA
28151 CTCCATCCAG CCCCAGGCAC GCCACCTGCT CCTGAGCCTC CACTATCTCC
28201 CTGTGACGGG TGAACCTCGT GTAGTGTGTC TCGGGTCCAT ATATGAATTG
28251 TGAGCAGGGT TCATCTATTT TAAACACAGA TGTTTACAAA ATAAAGATTA
28301 TTTCAAACCA CCGGTGTGGC TGCCTGGATG AGTCCTTGGG GGTAGGTCTC
28351 ACTCAGACCC TGGCAGTGAT GTGGGAGGGA GAGAGGCAGT GCTGGTAGAA
28401 GCAGCTCCAG AAGCAAAGGC AACAGCAGTA GAGTGACCAC GGAAGCGGCA
28451 AACATTGTCT TCCCTTCTCT ACCTTCCCTA GTGCCACCTG CAGGGAGGCC
28501 CAAAGCAAAG CCCCCTTGCC CTGCATTGGG CTGGCACTGC AGAAATAAGA
28551 TGAAACACAG TTATCGAGAG GATGCTGAAC ATCTATGAGC AGGTTTAAAA
28601 GCCAAGATGA GTCTCATCTG TTTGTGTGGG TCAGGAACGG GTCTTCTGTA
28651 AGGCATGAGG TGGGACTGGA TAATCTTTCA GATTGTGTGAT TGGATACCTC
28701 GGGGGAGCAG AGGCAGACTG GGATCTCAGG ACTGCAGGTA TTTCATACTT
28751 TGGGATATGG AATTGATGGA (SEQ ID NO:3)
```

FEATURES:

Start: 2044
Exon: 2044-2167
Intron: 2168-21554
Exon: 21555-21615
Intron: 21616-22462
Exon: 22463-22523
Intron: 22524-22974
Exon: 22975-23052
Intron: 23053-23711
Exon: 23712-23801
Intron: 23802-25392
Exon: 25393-25458
Intron: 25459-25613
Exon: 25614-25769
Stop: 25770

CHROMOSOME MAP POSITION:
Chromosome 14

FIGURE 3J



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ALLELIC VARIANTS (SNPs):

DNA			
Position	Major	Minor	Domain
206	-	T	Beyond ORF (5')
4963	C	T	Intron
8175	G	A	Intron
10515	T	C	Intron
13034	T	C	Intron
13781	T	C	Intron
14050	A	C	Intron
14273	-	T	Intron
17582	T	C	Intron
17700	C	T	Intron
18074	T	C A	Intron
19328	G	T	Intron
19570	A	G	Intron
20892	C	T	Intron
26465	G	A	Beyond ORF (3')
26472	A	G	Beyond ORF (3')
28071	C	T	Beyond ORF (3')
28096	C	G	Beyond ORF (3')
28403	A	G	Beyond ORF (3')
28467	C	G	Beyond ORF (3')

Context:

DNA

Position

206 GCTCAAGATTGCACAGCTGGTGAGTGGTGACACTGGGACTGGAACCCAAGTGTGCCTTAC
TCCAGAGCCCTTGGCATGCACCTGAAACCCCATGTAAGCCCACCTGTGGAGACGCGCACCT
CGAAATAATGGAATCCACTACATCAGTTCTCTTTAGCTTTCTGTGTAATCAGAGTAGCTAG
CAGGCTCGGGATTTCGCCCCCGGC
[-, T]
TTTTTTTTTTTTTTTTTTTGGAGACAGAGTTTTTGCTCTTGTTGCCCAGGCTGGAGTGCAAT
GGCGCAATCTCGGCTCACCGCAACCTTCGCCTCTCAGGTTCAAGCAATTCTCCTGCCTCA
GCCTCCCGAGTAGCTGGGATTACAGGCACCGGCCACCGCCAGCTAATTTTTTTATAT
TTTGTAGTAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTTGAACCTTTTCCCTCTT
ATTATAATTCAGACACTTAACCTGAAATATACCTTTTCAAATGAAGTAAATGGGCTTACC

(SEQ ID

NO:14)

4963 TATTAAGGGACTTGGGATTCTCCCTTATCTTGGGCGTGTTTTTCAGCATTAACATAAACT
TAAAGGAAAGAGTTGGATGGTCAAGAAAAGCTTTTTCCTTAAGTGATATGGACAGTTTCT
CAAGGAGGTAGAAGGGGCAGCCAGGAGACAAATCAAGGAGCCAACGAAATGAGTGTACCT
AAGTCATAGTCATTGCTTATTTTTAAAAAATGCGTGTCTGTATGCCAGGCTCTGCACT
GAGACCGAGAGATTCCAAGATGAATAATACCTACAGTCACTGTTCTCAAATTGTGCATTA
[C, T]
CTAAAACACATTACATGACCATGTGCGCCACTGATCGAGGCACCTTTCCCAGGGGCTTTT
TTTGTGAATTAAGAAAACAAGGTAATTCACCAAGTATTTGCAAGATAGTTTGGCTTCTTG
GCTCATGTGGATATCACCTAGGCCAGTACTTTTGTGATTTACTGTGTACTCCACTTTAAC
GGCCTGCGATCTTCTAGAGAAGAACCCGCCAGGGAGCAGTGAGAGGCCTCCCTGGTAGAC
TGAGACACTGACTGTCCCTCCCCCTATCCTTTTCTGCTTTTCTGGCCAGCAGACCAGCAGG

(SEQ ID

NO:15)

8175 ATGCCAGGTGCCATGCTAAGATTTGGGGACACAGTGGTGACCAAAACAGACAGAAACCAA

FIGURE 3K



Docket No.: CL001188
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GGAGCTGGCTTACATTCCAAGGGAGTGCATAGGAAGCTGTGTTTCATTTCAGTTTCTGCT
CTAGTACCCCCCTTTCCCTGGCAGTGCCAGGGTCTGAGAAGGAAGAGTGAGGTGGTGAGG
AGGTGTGAAGCAGTGGGGTGACCTGAGAGGAGAGGATGGGGTGGCTTTGCCTCAAGGCTT
GGGCCCTGCTAGGTGTGCTCTGCTCAGGCCTCTGTTTCTCCTCCTGACACAGGCACA
[G, A]
ACTCGCCTCCCACCCCTTCCCCAAGGACATGACCTTGGAAGGAACATATCTGAAGCCC
GCGGAGGGTTTCCGCTGCTGTGCATCTGTGCCACAGATCCGAGATGCACCCACAGCTGG
GAGCACCGGTTCTCCCGCTACCTGCACTCCCTGGTTTCTGTTCCCTCCTCCTCCTCT
TCCTTCTCCCCGCTCCCAGACAGGCTGGTGATGAGCTTTATAACATGAAAGCTGATATT
TGGCCATTATCCTTCTACCCTGATTGCCAGCTCTTCTCAGAGTGCCTTCTTCTGTAATCC (SEQ ID
NO:16)
10515 CTGGTGAAGGCTTTGAAGAGGAAGTGACATTTGAGTGGAGTCTTGAAGACTAGGCAGGAT
TCTCCAGGGGCCCTGGGTGTGGGGGAAGCACACATCCTCTTCCCTGTAGGAGGTGCTGTG
GAGAACACCTCCAGTGGGGCTGCTACTCTTCAGCCTTGCTGGGGCCAGCTGGAGTGGCCA
CACCATGGTACACCAGCTGAAGTTCAAGAAGCCCTTGCCAGGAGATTGCTTTGCTGGC
TCTGGGTGAGGGCAGGTGCATCTGGAAGCCCCCTTCTTCTAAGATGTTTGCTCCTGAGT
[T, C]
TCTATGTCCTAGTCTTTTCTTCCCTGAACCTTTTGCTACCAGTCAGCACAGCCCTGCCTG
AGAAGGAGGCTGGAGGAGTGAGTGGTCAGTAGCCTGGTGGGTCTTGCTGCCTCTGTGGT
GCCCCGTGGCCTAAGTAGCAGGCTTAGGGAGGCGAGACCCAGTTCAGGGGCTGCCAATG
GGGAGCGAGATGGGTGGCTGGAGCACACTGCACATGTACCAAGGCTCTAGGGAGGTCT
GTGCACAAGGCAGTGGGAAAAGCAAGGGGAAGACCCAGCCTGGTCAACATGGTGAAACCC (SEQ ID
NO:17)
13034 AGATTTGGGTGAGGACACAGCCAAACCATATCAGCTCCCGGATCCCTGTGTGAATGGGG
TCTTTTTTGGTGTGTTGAGGGCTGCACAGGGTGACCTCTTTAGAGGTGACCTCCTGCCACA
ACCCACAGGAGGTGCACATGGCCACACATGCTGGTTTCTGCACTGGGAGGGGCTGGGG
CACTCCTGGGACCTGTGCTTGGTAACTGGAGCTGGCCTGGCCCTGGGGATTGGGTGTCTG
CCTTGGGTTTTAGGTGTATTAGGTTTCTCCTCGTTGTGGAGTCTCATTACTAATGAAAG
[T, C]
TCAGGTGCGACTGCTGGTCCTTTGGGCTGTGGTTGATCCTGGTGATAACATTTGGCACCC
AGAGGCAGCCCTGTTTCCACTGAAGCATGCGGAGCTTGGCTGGCAGGCAGGCAAGCTGGC
AGCTGCCCTTAACCCATGAGGTGCTGGCCCGCTAGTAGGCACACCCCTACCTGTGCCAGAA
TTGAGGTTGTAGCCAGACTCCAGGAGCCATCTGGGCCCCACAGGGGGCGGCATTTCTCT
TTTTGTTGAAACATTCCAGCCAAGTGCTGGCTTGGGCTTCATCTCTGTGCCACTCTCC (SEQ ID
NO:18)
13781 CCCTGTGTTATGGGTTTTACACCTTATCTCACAATCTTAAAAAAAATTCTCTGAGAAT
CCTCTGTACCCCCACTTTACAGGTGAGGAAACTGAGGCAAAGATAGGCTAACTGGCTTC
CCCAACACCATGCAGGTAATTAGTGATAAAGGCAGGGTTGGAACCAAATTTGACCTCCCA
ATTGTGCTCTTAATGGCCAGGACACTCTGTGTCTTGAGCCACACTTCTCCATGTTTTCT
AGGGCTTTCTAGGGAGGCAGACAGTGATGGGAAGGGGTGTTCTTTAGTGTGGATGTGCCC
[T, C]
GCCTGCTCCTTTCTGTAAGCGTCACAGCACCTCCACTGCTGTACTGGGGAGGCACCAAGT
TTTTCCCTGTTTGGCCACCCAAAGGCGAGCTAGCTTAGGAGTCACGTGAGTGCTGGGTGTC
TCGCTGCTGCATCCCTCTATCCTGCCCCCTGCCCCGGTGCCAGAGGAGGGCCCTGCCT
GTCTTCCAGTTCTCCAACAGCAGCGCTGTCCAGCACCCCTCGGGCTCCAGTTGTGGCCT
GGCAGCTGCTGGGGCAGACACCATACAGACAGAGTCACAGCAGGAAGAGGATGGGGCCCA (SEQ ID
NO:19)
14050 GGAAGGGGTGTTCTTTAGTGTGGATGTGCCCTGCCTGCTCCTTTCTGTAAGCGTCACAGC
ACCTCCACTGCTGTACTGGGGAGGCACCAAGTTTTTCCCTGTTTGGCCACCCAAAGGCGAG
CTAGCTTAGGAGTCACGTGAGTGCTGGGTGTCTCGCTGCTGCATCCCTCTATCCTGCC
CTGCCCCCGGTGCCAGAGGAGGGCCCTGCCTGTCTTCCAGTTCTCCAACAGCAGCGCT
GTCCAGCACCCCTCGGGCTCCAGTTGTGGCCTGGCAGCTGCTGGGGCAGACACCATACAG
[A, C]
CAGAGTCACAGCAGGAAGAGGATGGGGCCAGGGCTGCTGCCTCAGGCCATGGCTGCATG
GCACCATCAGTTGATTGAGGAGCTTTCTTGCCAATGTCTGAGGCATCAGGTGGCAGAC
ACGTCTCCCTGCTCTTAAGCCTCAGGCATGCAGCCCTTCTTATGCTCTCTGGGGTGAGGG

FIGURE 3L



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GGAGATCCCCCTCATGGAATTGCTTTTTTTTTTTTTTTTTTTTTTTTGGAGACAGGGTCCT
GCTCTGTCACTCAGGCTGGAGTGCAGCCTCAACCTCCCAGACTCAAGTGATCCTCCTGCC (SEQ ID
NO: 20)

14273 TCTCCAACAGCAGCGCTGTCCCAGCACCCCTCGGGCTCCAGTTGTGGCCTGGCAGCTGCTG
GGGCAGACACCATACAGACAGAGTACAGCAGGAAGAGGATGGGGCCAGGGCTGCTGCC
TCAGGCCATGGCTGCATGGCACCATCAGTTGATTGAGGAGCTTTTCTTGCCAATGTCTGA
GGCATCAGGTGGCAGGACACGTCTCCCTGCTCTTAAGCCTCAGGCATGCAGCCCTTCTTA
TGCTCTCTGGGGTGAAGGGGAGATCCCCCTCATGGAATTGCTTTTTTTTTTTTTTTTTTTT
[-, T]
TTTTGAGACAGGGTCCTGCTCTGTCACTCAGGCTGGAGTGCAGCCTCAACCTCCCAGACT
CAAGTGATCCTCCTGCCTCAGCCTCCCGAGTAGCTGGGACCACAGGTGGACACCATCACA
CCTGGGTTTTTTTTGTTTTTGTCTTTTGTCTTCTAGAGATGGGGTCTCACTTTCTTGCTC
AGTCTGGTCTCGAACTCCTGGGCGCAAGCAGTCTCCACCTCGTCTTCCCAAAGTGTTT
GGATTACAGGTGTGAGCCACTGTGCTTGGCCTTTTATTTATTTAGAAATTTGTTTTGGAA (SEQ ID
NO: 21)

17582 GGATGTTTTCTTCCATGACATATATAGCTCTTGAACTACTTCTATCTAATATACCCACA
GTGCTGTTAAAAATACAGATTTCTGGGCCTCACCTCAAATTATGATTCAGTAGGTCTAG
GCACGTCAAGGTCAATTGTTTTTGTCTTTGTTTTAAGTCACCCCAGGTGATTCTAAAGCCG
AAGCTCTGCAAAGCACACCTTGAGAAACAGAGAACTCTGTGCTCTCGCTCTCTTGACAC
TTCAGGTGCAAACTTTTGTCTTAATGTCTTCTCAAACCTACGCATGTGTGAGAATCAC
[T, C]
GTGAGAGCTTATTGAACTGATTGCGGGACCCCATACCTAGAGGGCCTGATTCTATAGGT
CTGAGGTAAGGCCCAAGAATTTGCATATTTGCATTTCTGTTTTCTTTCTTTCTTTCTTT
TTTTTTTTTTTTTGTGAGATGAAGTCTCACCTGTGCGCCAGACTGGAGTGCAGTGGCATGA
TCTCAGCTCACTGCAGCCTCTGCCTCCTGGGTTAAAGCGATTCTCCCCACACCCAGACC
CGCTCCTGAGTAGCTGGGATTACAGGTGCGCCGCCACCATGACTAGCTAACGTTTGTATTT (SEQ ID
NO: 22)

17700 AGGCACGTCAAGGTCAATTGTTTTTGTCTTTGTTTTAAGTCACCCCAGGTGATTCTAAAGC
CGAAGCTCTGCAAAGCACACCTTGAGAAACAGAGAACTCTGTGCTCTCGCTCTCTTGAC
ACTTCAGGTGCAAACTTTTGTCTTAATGTCTTCTCAAACCTACGCATGTGTGAGAATC
ACTGTGAGAGCTTATTGAACTGATTGCGGGACCCCATACCTAGAGGGCCTGATTCTATA
GGTCTGAGGTAAGGCCCAAGAATTTGCATATTTGCATTTCTGTTTTCTTTCTTTCTTTT
[C, T]
TTTTTTTTTTTTTTTGTGAGATGAAGTCTCACCTGTGCGCCAGACTGGAGTGCAGTGGCAT
GATCTCAGTCACTGCAGCCTCTGCCTCCTGGGTTAAAGCGATTCTCCCCACACCCAGAC
CCCGTCTAGTAGCTGGGATTACAGGTGCGCCGCCACCATGACTAGCTAACGTTTGTAT
TTTTAGTAGAGACGGGGTTTTCCCATGTTGGCCAGGCTGGTCTCAAACCTCCTGACCTCA
GGTGATCCACTCACCTCAGCCTCCCAAGGTCTTGGGATTACTGGTGTGAGCCACCGCGTG (SEQ ID
NO: 23)

18074 TGCAGCCTCTGCCTCCTGGGTTAAAGCGATTCTCCCCACACCCAGACCCGCTCCTGAGT
AGCTGGGATTACAGGTGCGCCGCCACCATGACTAGCTAACGTTTGTATTTTAGTAGAGAC
GGGGTTTTACCATGTTGGCCAGGCTGGTCTCAAACCTCCTGACCTCAGGTGATCCACTCA
CCTCAGCCTCCCAAGGTCTTGGGATTACTGGTGTGAGCCACCGCGTGCGGCCAGAATTTG
CATTTCTAACAAGTCCCAGGTGATGCTGATGCTGTGGGTCCAGGGACACACTTTGAGAAC
[T, C, A]
GCTTGTTACTCAGGCGATATGTGGACAGTAGCGTCATCTTACCTGGGAGCTTCTGCGAG
CATCTCAGGCCTTGCCCTACACCTACCAGATCAGAATCTGCATTTTAACTCAATCCCCGC
GTGATTCTCATGCACCTGGAAGTTTGAGAAATATGACCTTAGAGGAGCCGGAATGTGAAA
CCACTGGAGGCAGAGATAGATGGAGAATATCTCTTCTCTCAGGATACTAAAGATGCAA
CAAAAAGGGCTGACTCTCTGGGTGTGCACCCAGGTGGGGCTGATGACCGAAAAGAGGCCA (SEQ ID
NO: 24)

19328 TGTGTGTGAGGCCGGGGAGTGCTGCGAGCCCCGGAATTCCTCAGCCTTAGTCCCCCGCCA
CATAGCTAAGAAGTGAGGGAGGAGGTGAGAAGGAGTCACTGCCAGCCTCACTTCCGGTG
GAGTACCTCTCCTTGTCAAGTTCTGTCTCTGGGGACAGTTGCCCTGCTTTACCTCTCC
CTCCATCCCCCTCTCTCTCACAGGGAAAAATTACCTTAATATTGGAAGTTCTCTCCTA

FIGURE 3M



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GCAAAGTCCTTCTCAGGCACCCACAGGCAAAAAGGAACTAAGCAGAGTTAGGGCTTCCA
[G, T]
GCCTAGCCAACTACACGACTCTCCTCTTGCTTCCCTAAGAACCAGCGCAAGGGGCAGCGT
GGGTTCAGCATAGATGGACCTGTGTTGGAATCTCTGCACGTGCTGTGCTGACCTGGCT
AGCCATTGACCTCTCTGAGCCCTTGTTTCCCTTCCACTAGGCTCTCTGAGGGCAGGGGCC
ATGCTTTTTCTACTGCTCTGTCTGCACTGAGCACTGTGCAGGGCACATAGGAAGTTCCCA
TAAATGTTTGTGGGATAAAGGAAATAAAACCTTCTCTCTTCTGTCCTTGTGATGGC (SEQ ID
NO:25)
19570
AAAGTCCTTCTCAGGCACCCACAGGCAAAAAGGAACTAAGCAGAGTTAGGGCTTCCAGG
CCTAGCCAACTACACGACTCTCCTCTTGCTTCCCTAAGAACCAGCGCAAGGGGCAGCGTG
GGTTCAGCATAGATGGACCTGTGTTGGAATCTCTGCACGTGCTGTGCTGACCTGGCT
GCCATTGACCTCTCTGAGCCCTTGTTTCCCTTCCACTAGGCTCTCTGAGGGCAGGGGCCA
TGCTTTTTCTACTGCTCTGTCTGCACTGAGCACTGTGCAGGGCACATAGGAAGTTCCCAT
[A, G]
AATGTTTGTGGGATAAAGGAAATAAAACCTTCTCTCTTCTGTCCTTGTGATGGCTT
TGCACAAGGCACTGTCTTGGCCAGGTTTGCTAGGCTAGTGTGAGGATAAACCAGGTATA
TTACAAATTGGAGAAAATTTCTCGTTCTTCTTGGAGAAGGTGCTGTATCATGAAACAAG
AATGCTTTGATTCCCTTCTATGCCAGGTACTGGGGAGAAAACAGGTGCCTGATAACCGTTG
ATCCAGGCAGAAATAAGCATACTCCTGCTTCCCAAGGCCTGATGCTTCTCTCTTCTCTCC (SEQ ID
NO:26)
20892
CCTTGGATGAAGAAGCGTGGGAACCTTTGCTTCCCTTCCCTCCCGCAGTGACATGCCAT
GCCATGCCACTGCCCTCTTCATCTGGTCCCTATGACAGTCACTCATAAGCACCCGCATGTAC
CCGGCCCTGCACTAGCTCATGACAGCTGCAGTCAATTGGGCCAGGTGCTGTATCTCATCC
GGCCTCCTCAGCAACCCCTCTGAGATACTGGTAATGTCCCTGATGAAGATATTTACTGAGG
CAGAAATGGACGCTCAGTGAAGCAAGGTGCCTGATGTTATAGCAATGAGCTATGAGTGGC
[C, T]
AGAGGGAGGAGATAAGCTCAGGCCTGACACCAAAGCCCATGCTCCTTCTAGTCAACCACA
GTGCCCTCCTATGGTGAATGAGTGAGTCAGCAACCAAGACGCATGAGGCCTTCTTTTTGGT
GAGCCTTGGCTGGGTGCTGAGGCTTCAAGGTACAATCATGGGTGGAAGAGCCCTCCTCTC
TCTCCACAGTCTGGCACTATGACCCTTCTGTTATTAACAAGGCAAAGAGAGAGAGGGA
AGAAAGCAGGCAAAATAATGTGGTTGCTATTCTAGAGATTAGAATTTTCAGGAAGGATAA (SEQ ID
NO:27)
26465
TTCTCTGACCCCTCCCTCCGGTGCCTTTTCGTATCAAAGCTCCTCAAACCCCGTCCCCCG
TGTGTCCTGCTGTGTGCAGCTCGCTCTTTCTTCTTCTTAAGCTATCCAAGGGGATGGA
CCAGGCTCGTGGGAGGTTCCACCCTTGGATCCAGGAAGAACCCTCCACCCTGCCTCGT
GGGTGGGCTCAAAGGCTACAGGGTGCTTCTTCTCTTCCCCCACCCTCATGTCCCTCATG
TGCCATGGGCCTGCCTCCCCAGTGACCTGCGAAAGTGGAGCATCGAGGTAGGAGGGAAAC
[G, A]
GCAACCAGGGAGTCTCTGAGCCTGGGGCTGCCCTACCTCTACCCATTCCCCGACCAGAGC
TTTGCCCTTGCTTGCTGCCCCGCTGCTCTTTGGGGAAGTGAAGCTCAGAGGCAGGTGCT
TCAGAGAAGGAAACAAAATGAGGGGTGGCAGGGATAAAAAGTCACCTCCATTCTCTACCT
CCCATGCAGCATGAACACAATTTCTCTCCACCTGGCTCCCAAATTTAAAGATGTGGACCA
AGGCCTGTGGGTACTCCAGGGGCAAGGAGAGCCCTGGGGTCAGTGACACTGTGAGGCCAA (SEQ ID
NO:28)
26472
ACCCCTCCCTCCGGTGCCTTTTCGTATCAAAGCTCCTCAAACCCCGTCCCCCGTGTGTCC
TGCTGTGTGCAGCTCGCTCTTTCTTCTTCTTAAGCTATCCAAGGGGATGGACCCAGGC
TCGTGGGAGGTTCCACCCTTGGATCCAGGAAGAACCCTCCACCCTGCCTCGTGGGTGGG
CCAAAGGCTACAGGGTGCTTCTTCTCTTCCCCCACCCTCATGTGCCATG
GGCCTGCCTCCCCAGTGACCTGCGAAAGTGGAGCATCGAGGTAGGAGGGAAACGGCAACC
[A, G]
GGGAGTCTCTGAGCCTGGGGCTGCCCTACCTCTACCCATTCCCCGACCAGAGCTTTGCC
TTGCTTGCTGCCCCGCTGCTCTTTGGGGAAGTGAAGCTCAGAGGCAGGTGCTTCAAGAGA
AGGAAACAAAATGAGGGGTGGCAGGGATAAAAAGTCACCTCCATTCTCTACCTCCCATGC
AGCATGAACACAATTTCTCTCCACCTGGCTCCCAAATTTAAAGATGTGGACCAAGGCCTG
TGGTACTCCAGGGGCAAGGAGAGCCCTGGGGTCAGTGACACTGTGAGGCCAACCATGCA (SEQ ID
NO:29)

FIGURE 3N



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28071 GCCAGGGACTTGAGAAGTTATATTGGGCAGTGGCTCCAATCTGTGGACCAGTATTTTCAGC
TTTCCCTGAAGATCAGGCAGGGTGCCATTTCATTGTCTTTCTCTCCTAGCCCCCTCAGGAA
AGAAGGACTATATTTGTACTGTACCCTAGGGGTTCTGGAAGGGAAAACATGGAATCAGGA
TTCTATAGACTGATAGGCCCTATCCACAAGGGCCATGACTGGGAAAAGGTATGGGAGCAG
AAGGAGAATTGGGATTTTAGGGTGCAGCTACGCTCACCTAAACTTTTGGTGGCCTGGGG
[C, T]
ATGTCTTGAGGCCCAGACTGTTAACCAGGCTCTGCTGGCCTGTTTACTCGTCACCACCTC
TGCACCTGCTGTCTTGAGACTCCATCCAGCCCCAGGCACGCCACCTGCTCCTGAGCCTCC
ACTATCTCCCTGTGACGGGTGAACCTCGTGTACTGTCTCGGGTCCATATATGAATTGT
GAGCAGGGTTCATCTATTTTAAACACAGATGTTTACAAAATAAAGATTATTTCAAACCAC
CGGTGTGGCTGCCTGGATGAGTCTTGGGGTAGGTCTCACTCAGACCCTGGCAGTGATG (SEQ ID
NO:30)

28096 GGCAGTGGCTCCAATCTGTGGACCAGTATTTTCAGCTTTCCCTGAAGATCAGGCAGGGTGC
CATTTCATTGTCTTTCTCTCCTAGCCCCCTCAGGAAAGAAGGACTATATTTGTACTGTACC
CTAGGGGTTCTGGAAGGGAAAACATGGAATCAGGATTCTATAGACTGATAGGCCCTATCC
ACAAGGGCCATGACTGGGAAAAGGTATGGGAGCAGAAGGAGAATTGGGATTTTAGGGTGC
AGCTACGCTCACCTAAACTTTTGGTGGCCTGGGGCATGTCTTGAGGCCCAGACTGTTAA
[C, G]
CAGGCTCTGCTGGCCTGTTTACTCGTCACCACCTCTGCACCTGCTGTCTTGAGACTCCAT
CCAGCCCCAGGCACGCCACCTGCTCCTGAGCCTCCACTATCTCCCTGTGACGGGTGAAC
TCGTGTACTGTGTCTCGGGTCCATATATGAATTGTGAGCAGGGTTCATCTATTTTAAACA
CAGATGTTTACAAAATAAAGATTATTTCAAACCACCGGTGTGGCTGCCTGGATGAGTCCCT
TGGGGTAGGTCTCACTCAGACCCTGGCAGTGATGTGGGAGGGAGAGAGGCAGTGCTGGT (SEQ ID
NO:31)

28403 CTGCTGGCCTGTTTACTCGTCACCACCTCTGCACCTGCTGTCTTGAGACTCCATCCAGCC
CCAGGCACGCCACCTGCTCCTGAGCCTCCACTATCTCCCTGTGACGGGTGAACCTCGTGT
ACTGTGTCTCGGGTCCATATATGAATTGTGAGCAGGGTTCATCTATTTTAAACACAGATG
TTTACAAAATAAAGATTATTTCAAACCACCGGTGTGGCTGCCTGGATGAGTCCCTGGGGG
TAGGTCTCACTCAGACCCTGGCAGTGATGTGGGAGGGAGAGAGGCAGTGCTGGTAGAAGC
[A, G]
GCTCCAGAAGCAAAGGCAACAGCAGTAGAGTGACCACGGAAGCGGCAAACATTGTCTTCC
CTTCTCTACCTTCCCTAGTGCCACCTGCAGGGAGGCCCAAAGCAAAGCCCCGTTGCCCTG
CATTGGGCTGGCACTGCAGAAATAAGATGAAACACAGTTATCGAGAGGATGCTGAACATC
TATGAGCAGGTTTTTAAAGCCAAGATGAGTCTCATCTGTTTGTGTGGGTCAGGAACGGGTC
TTCTGAAGGCATGAGGTGGGACTGGATAATCTTTCAGATTGTGATTGGATACCTCGGG (SEQ ID
NO:32)

28467 GCACGCCACCTGCTCCTGAGCCTCCACTATCTCCCTGTGACGGGTGAACCTTCGTGTACTG
TGTCTCGGGTCCATATATGAATTGTGAGCAGGGTTCATCTATTTTAAACACAGATGTTTA
CAAAAATAAAGATTATTTCAAACCACCGGTGTGGCTGCCTGGATGAGTCCCTGGGGGTAGG
TCTCACTCAGACCCTGGCAGTGATGTGGGAGGGAGAGAGGCAGTGCTGGTAGAAGCAGCT
CCAGAAGCAAAGGCAACAGCAGTAGAGTGACCACGGAAGCGGCAAACATTGTCTTCCCTT
[C, G]
TCTACCTTCCCTAGTGCCACCTGCAGGGAGGCCCAAAGCAAAGCCCCGTTGCCCTGCATT
GGGCTGGCACTGCAGAAATAAGATGAAACACAGTTATCGAGAGGATGCTGAACATCTATG
AGCAGGTTTTTAAAGCCAAGATGAGTCTCATCTGTTTGTGTGGGTCAGGAACGGGTCTTCC
TGAAGGCATGAGGTGGGACTGGATAATCTTTCAGATTGTGATTGGATACCTCGGGGGAG
CAGAGGCAGACTGGGATCTCAGGACTGCAGGTATTTTCATACTTTGGGATATGGAATTGAT (SEQ ID
NO:33)

FIGURE 30